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Page

3480 3000 3060 3120 3180 3240 3300 3360 3420 3540 3600 3660 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 2940 653 664 684 704 724 744 764 784 804 824 844 864 884 904 APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Lodes, Michael J.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Woweill, Patricia D.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer GCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCAAAGC ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla LeuProThrHisAspProSerProLeuGlnArqTyrSerGluAspProThrValProLeu 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu --GlnAsnGluAspLeuGlyProAlaSerProLeu 919 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal

			20	40 120	60 180	80 240	100 300	120 360	140 420	160 480	180 540	200	220 660	240 720
IER-2/NEU-ASSOCIATED MALIGNANCIES 44. RR: US/09/930,125 01-08-14 idows Version 3.0	Length: 3768 0.00 Matches: 919 0.08 Conservative: 0 0.3% Mismatches: 336 0.9% Indels: 1	5-1 (1-3768)	aLeuCysArgTrpGlyLeuLeuAlaLeuLeuBroProGlyAla 	AlaSerThrGlnValCysThrGlyThrAspWetLysLeuArgLeuProAlaSerProGlu 	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 	GlubeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspileGlnGluVal 	GInGlyTyrvalLeuileAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 	ASPProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 	GinLeuargSerLeuThrGluileLeuLysGlyGlyValLeuileGlnargAsnProGln 	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 	AlaglyGlyCysAlaArgCysLySGlyProLeuProThrAspCySCySHisGluGlnCyS
LE OF INVENTION: OF HER- S. REFERENCE: 210121.544 ERNT APPLICATION NUMBER: RENT FILING DATE: 2001-(BEN OF SEQ ID NOS: 25 IWARE: FastSEQ for Window ID NO 1 ID NO 2016 ID NO 3016	res: 0 4900.00 arity: 73.23% mllarity: 73.23% 10.49%	x US-09-930-125	MetGluLeuAlaAlaLeuCysArg' 			GlubeuThrTyrbe			AspProLeuAsnAs 	GinLeuArgSerLe 	LeuCysTyrGlnAs 			AlaGlyGlyCysAl GCCGGTGGCTGTGC
FILE REFERENCE: CURRENT APPLICAT CURRENT APPLICAT CURRENT FILING D NUMBER OF SEQ ID SOFTWARE: FASTSE SEQ ID NO 1 LENGTH: 3768 TYPE: DNA ORGANISM: HOMO FEATURE: NAME/KEY: CDS LOCATION: (1) US-09-930-125-1	Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match:	SEQ6 (1-919)	Qy 1 Db 1	Qy 21 Db 61	Oy 41 Db 121	Oy 61 Db 181	Qy 81 Db 241	Qy 101 Db 301	Qy 121 Db 361	Qy 141 Db 421	Qy 161 Db 481	Qy 181 Db 541	Qy 201 Db 601	Qy 221 Db 661

ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu g P Db g g οy g g Qy Db οχ D Dp a g δŽ Ω g QQ d g ò d δ δy ò δ δy οy οy ò Qγ οy ογ Ω

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; SEQ ID NO 1 ; LENGTH: 3768 ; TYPE: DNA ; ORGANISM: Homo sapien ; FRATURE: ; LOCATION: (1)(3765) US-10-313-644-1	J. No.: 0 00.00 1. No.: 4900.00 ent Similarity: 73.23% L. Local Similarity: 73.23% ry Match: 12.49%	SEQ6 (1-919) x US-10-313-644-1 (1-3768) QY	Db 61 GCGAGCACCCAAGTGTGCACCGCACAGACATGCGGCTCCCTGCCAGTCCCGAG 120	181 GAACTCACCTACCACCAACCAGCCTGTCCTTCCAGGATTATCCAGGAGGTG 24 81 GInGlyTyrValLeullealaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 10	uleu 1	161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnasuGlnLe 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnasuGlnLe 161 [1111111111111111111111111111111111	TATGTHATOR 10 S S S S S S S S S S S S S S S S S S

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0 4900.00 73.23% 73.23% 96.49%	-411-5 (tGluLeuAlaAlaLeuCy. 	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuPr	AAGTGTGC	SpMetLeu 	/rLeuPro 	alteulle 	eValArgGlyThrGlnLeuPheGluAs	SCACCCAG	AspProLeuAsnAsnThrThrProVa 	gSerLeuThro	년 -	AGGACACG	hrLeuIleAspThrAsnArgSerAr. 	CysTrpGly(799;	CysalaargCys 	AlaAlaGlyCysThrGly	scaceeec	rsGluLeu srGAGCTG	snProGlu	54577716	rrasnTyrLeuSerThrAspValGlySerCysThrLeuvalC;
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ent Sco No.: t Simil Scal Si Match:	1-919)	1	21	235	41 295	61 355	81	0 1	_	121 535	141	161	655	181 715	0	_	221 835		895	261	281	4 6	301
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ATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCCAGCAG 2214 1435 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCAAATGGCGCC 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe oy D g Oy Dp Oy Db Oy Db Qy qq Q 0y 0y 0b g g Op 엄 g g Dp QΥ Dp οy g δý Óγ Q Qγ Ω ò δ

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qq	235 GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCGAGTCCCGGG 294	a i	
ΟŸ	ThrHisteuAspWetLeuArgHisteuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 6	à a	401 GIUTAFLEUC 1375 GAGACTCTGC
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qq	2335 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2394	Db 3415 GCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCAAAGC 3474
٥y	653 653	765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 7
qq	2395 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2454	3475 CTCCCCACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTG
Qy	653 653	785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 8
QQ	2455 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGGGCTCCCCCA 2514	3535 CCCTCTGAGACTGATGGCTACGTTGCCCCCTGACCTGCAGCCCCCAGCCTGAATATGTG
Qy	653 653	003 ASIIGLIRTOASDVALALGYTOGIIRTOYLOSGIYLOALGYLUGIYYYLOGGURTOALGALAALA
qq	2515 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2574	3353 AACCAGCCAGATCAGCCCCCAGCCCCCTTCGCCCCGGAGAGGGCCCTCTGCTGCC
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οy	653 653	Oy 845 VallysAspValPheAlaPheGlyGlyAlaValGluAsnPrOGluiyrLeuThrPrOGlu 864
QQ	2635 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694	5/15 GICHARGACGIIIIIGCCIIIGGGGGGGGGGGGGGGGGGGGGGG
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Οy	653 653	905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
qq	2815 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2874	3895
Qy	653 653	RESULT 6 US-10-146-473-32
qq	2875 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGGCTGATGACTTTTGGGGCC 2934	; Sequence 32, Application US/10146473 ; Publication No. US20030108888A1
οy	653 653	; GENERAL INFORMATION: ; APPLICANT: Scanlan, Matthew
QQ	2935 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCAAAAGGGGGGAGCGG 2994	; APPLICANT: Gout, Ivan ; APPLICANT: Stockert, Elisabeth
٥y	653 653	; APPLICANT: Gure, Ali ; APPLICANT: Chen, Yao-Tseng
qq	2995 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCGAAATGTTGGATG 3054	; APPLICANT: Old, Lloyd ; TITLE OF INVENTION: Breast Cancer Antigens
0y	653 653	; FILE REFERENCE: LO0461/70130(JRV) ; CURRENT APPLICATION NUMBER: US/10/146,473
qq	3055 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCGCATGGCC 3114	; CURRENT FILING DATE: 2002-15-15; PRIOR APPLICATION NUMBER: US 60/291,150
Οy	654 654	; PRIOR FILING DATE: 2001-05-15 ; NUMBER OF SEQ ID NOS: 82
qa	3115 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 32
Qy Db	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	S
ΟŸ	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704	nment Scores:
QQ	3235 GAGGAGTATCTGGTACCCCAGCACACGCTTCTTCTGTCAGACCCTGCCCCGGGCGCTGGG 3294	0 Length: 4900.00 Matches:
Qy	705 GlymetValHisHisArgHisArgSerSerSerSerGhrArgSerGlyGlyGlyAspLeuThr 724 	Percent Similarity: 73.23% Conservative: 0 Best Local Similarity: 73.23% Mismatches: 0 Query Match: 96.49% Indels: 336 DB: 14 Gaps: 1
οy	725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744	SEQ6 (1-919) x US-10-146-473-32 (1-4473)
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CGACCTGCTGGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGTC 3714
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Publication No. US20030118592A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOCLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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Mismatches:
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APPLICANT: Elizabeth Singer
APPLICANT: Raif Landgraf
APPLICANT: Raif Landgraf
APPLICANT: Raif Landgraf
APPLICANT: David Eisenberg
TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
FILE REFERENCE: 30448.103-U5-U1
CURRENT APPLICATION NUMBER: 05/10/207,498
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/308,431
PRIOR APPLICATION NUMBER: 60/308,431
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                 61 GCGAGCACCCCAAGTGTGCACCGGCACAGAAAACTGCGGGCTCCCTGCCAGTCCCGAG 120
                  3655 CGACCTGCTGGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCCAGGGAAGAATGGGGTC
                                                            GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu
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; Sequence 5, Application US/10207498
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; GENERAL INFORMATION:
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                                                 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG
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2341 TATGTCTCCGCCTTCTGGGCATCTGCCTGACAI	qa	61 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGACTTCTTGCAAGTTCTTGCAAGTAATGCCGCC 13
	Qy	2] AsoleniSerValPheGlnAsnLenGlnValIleArrdClvArrIleLenHieBerGlvAla AA0
2281 CCCAAAGCCAACAAAAATCTTAGACGAAGCAT	Z Q	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCAA	qa io	
653	Qy	PheAsp6]vAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGLuGlnAalphe 400
2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTT	qa	41
	Qy	11eGlnGlupheAlaGlvCvsivsIvsIvsIlepheGlvSerienAlapheInproGluSer 380
2101 ACACCTAGCGGAGCGATGCCCAAACCAGGCGCAGA	qa	34 VALCESTYLOLY EUGLINGE CHURISLEUARGELUVALARGALAVALTTISERALASIN 360
653	δλ	UNIO LA CALCACACACACACACACACACACACACACACACAC
2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGC	qa	321 G10ValThrAlaGluAspGlyThrGlnArgCysGluLysCysScrLysProCysAlaArg 340
653	Qy	INCARCIALITICIACEGRACEIGEGRAICCIGECACCALICACCACCACCACCACAACCAAA
81 ATTCTGCTGGTCGTGG	ga qa	301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
1341 GGC1GCCCCCCAGCAGAGAGCCAGCCC1C1C1CAGCCC1C1C1CAGCCCAGCCCAGCCC1C1CAGCCCAGCAG	20 20	841 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGTG
641 GlyCysProAlaGluGlnArgAlaSerProLeuT	δλ	ArgTyrThrPheGlyAlaSerCysValThrAlaC
1861 GGGGGATGCCAGCCTTGCCCCATCAACTGCACCC	qq	201 Sefectylecyschiedentskystroalaleuvalintrytashinraspinfysfell 280
621 GlyAlaCysGlnProCysProIleAsnCysTh	δλ	ZI GUIGUCGGCTIGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTG
	÷ 8	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 26
1/41 GCTGACCAGTGTGTGGCCCTGTGCCCACTATAA	g :	661 GCCGGTGCCTGTGCCCCCTGCAAGGGCCCACTGCCTGCTGCTGCCTGC
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1681 TTGCCGTGCACCTGAGTGTCAGCCCCAGAAT	් යි	201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
561	3 0	CTCACACTGATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAA
541 ValGluGluGysArgValLeuGlnGlyLeuProA	9y 4d	20
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1501 GAGGACGAGTGTGTGGGCGAGGGCCTGGCCTG	g :	421 CAGCTTCGAAGCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
501 GluAspGluCysValGlyGluGlyLeuAlaCysH 	δλ	17
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481 ProTrpAspGlnLeuPheArgAsnProHisGlnA	δλ	AspProfemenAsnThrThrDroValThrGlvAlaSerProGlvGlvClvIem11
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461 LeuGlySerGlyLeuAlaLeuIleHisHisAs	Qy	

CACCCACCTCTGCTTCGTGCACACGGTG 1440 rHisSerCysValAspLeuAspAspLys 640 TGGGATCCTCATCAAGCGACGCAGCAG 2040 CATCAAAGTGTTGAGGGAAAACACATCC 2280 ATACGTGATGGCTGGTGTGGGCCTCCCCA 2340 ATCCACGGTGCAGCTGGTGACACGCTT 2400 nalaLeuLeuHisThralaAsnargpro 500 SHISGInLeuCysAlaArgGlyHisCys 520 SSerGlnPheLeuArgGlyGlnGluCys 540 SASPProProPheCysValAlaArgCys 600 EProlleTrpLysPheProAspGluGlu 620 SCAGGAAACGGAGCTGGTGGAGCCGCTG 2100 SATGCGGATCCTGAAAGAGACGGAGCTG 2160 FGGCACAGTCTACAAGGGCATCTGGATC 2220 GGAAAACCGCGGACGCCTGGGCTCCCAG 2460 9 653 653 480 ThrHisLeuCysPheValHisThrVal uThrSer----

AGTGGCATCTGTGAGCTGCACTGCCCAGGTCACCTACAACACAGACACGTTTGAG 840 SerWetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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sncysSerGlnPheLeuArgGlyGlnGluCys 540 TCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040 AAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2340 LacysHisGlnLeuCysAlaArgGlyHisCys 520 CGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160 CTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220 TGACATCCACGGTGCAGCTGGTGACACAGCTT 2400 TCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460 653 653 TGCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2100 653 TGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280 653 653 CCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520 isGlnAlaLeuLeuHisThrAlaAsnArgPro 500 roLeuThrSer

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GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
3601 GGAGGAGCTGCCCCTCAGCCCCACCCTCCTGCCTTCAGCCCAGCCTTCGACAACCTC
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                                               TRANSGENIC NON-HUMAN TUMOR MODEL
                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                        APPLICANT: Erickson, Sharon
APPLICANT: Schwall, Ralph
APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
FILE REFERENCE: GENENT.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SCOTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                       (1-919) x US-09-811-115-2 (1-3768)
                                                                                                 Sequence 2, Application US/09811115
Patent No. US20020035736A1
GENERAL INFORMATION:
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Pred. No.:
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                                                                        1641 GGGGGCAAGGTGCCCATCAAGTGGATGCCCTGGAGTCCATTCTCCGCCGGCGGTTCACC
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LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 20	Qy	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
GTAA alCy 	QY	561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 24 [Qy	581 AlaAspGlncysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeutisPheAsnHis 26 [Qy	601 ProserGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620
SerGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 28	qa O	621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 30	QY Db	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 	Qy Dp	653
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ValcysTyrGlyLeuGlyWetGlUHisLeuArgGluValArgAlaValThrSerAlaAsn 3	QY	653
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GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpFroAspSerLeuPro 420	Qy	53
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441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460 	QA Dp	53 65. 01 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGGCTCCCAG 24.
461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCySPheValHisThrVal 480 	QQ Dp	53
481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500 	λο -	653
GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	Qy	653
1501 GAGGACGAGTGTGTGGGCGAGGCCTGCCACCAGCTGTGCGCCCGAGGGCACTGC 1560	DD OY	2581 ATTACAGACTTCGGGCTGGCTGCTGCTGGCATTGACGAGACAGGGCATGCAGAT 2640 653

ପ	2641 GGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCCGGCGGTTCACC 2700	Db 3721 CCTACGGCAGAGAACCCAGAGTAC
Qy	. 653 653	RESULT 11 US-09-877-177-11
q	2701 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGAGCTGATGACTTTTGGGGCC 2760	; Sequence 11, Application US/09877177 ; Publication No. US20020192652A1
ογ	653 653	; GENERAL INFORMATION: ; APPLICANT: Peter V. Danenberg et al
qq	2761 AAACCTTACGATGGGATCCCAGGCCGGGAGATCCCTGACCTGGTGGAAAAGGGGGGAGCGG 2820	; TITLE OF INVENTION: Method of deter; ; TITLE OF INVENTION: Factor Recepto
ογ	653 653	FILE REFERENCE: 11220/120; CURRENT APPLICATION NUMBER: US/09/8
qq	2821 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATGATGTTGGATG 2880	CURRENT FILING DATE: 2001-06-11; NUMBER OF SEQ ID NOS: 11
ογ	653 653	; SOFTWARE: FastSEQ for Windows Versi; SEQ ID NO 11
QQ	2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCGAATTCTCCCGCATGGCC 2940	
Qy	654	ORGANISM: Homo sapiens US-09-877-177-11
qq	2941 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	Alignment Scores:
Οy	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	4892
QQ	3001 GACAGCACCTICTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3060	Best Local Similarity: 73.158
oy	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	10
QQ	3061 GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCGGGCGCTGGG 3120	SEQ6 (1-919) x US-09-877-177-11 (1-453
δ i	GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyGlyGlyBleuThr	٦
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δ	745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGlyLeuGlnSer 764	Oy 41 ThrHisLeuAspMetLeuArgHis
qa	3241 GCTGGCTCCGATGTATTGATGGTGACCTGGGAATGGGGGCCAGCCA	Db 271 ACCCACTGGACATGCTCCGCCAC
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qa	CCCTCTGAGACTGATGCTACGTTGCCCCCCTGACCTGCAGCCCCCAGCCTGAATGGTG	UY 81 GINGLYTYVALLEBULLEALAHIS. DD 391 CAGGGCTACGTGCTCATCGCTCAC.
Qy	805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824	Qy 101 IleValArgGlyThrGlnLeuPhe
qq	3421 AACCAGCCAGATGTTCGGCCCCCAGCCCCCTTGGCCTCTGTGTGTG	Db 451 ATTGTGCGAGGCACCCAGCTCTTT
λΌ	825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLySAsnGlyVal 844	Qy 121 AspProLeuAsnAsnThrThrPro
qa	3481 CGACCTGCTGCTGCCACTCTGGAAAGGCCCAAGACTCTCCCCCAGGGAAGATGGGGTC 3540	Db 511 GACCGCTGAACAATACCACCCT
Qy	ValLysAspVa	Qy 141 GlnLeuArgSerLeuThrGluIle
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ΟŊ	885 TyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904	Oy 181 LeuThrLeuIleAspThrAsnArgi
qq	TATTACTGGGAC	Db 691 CTCACACTGATAGACACCAACGGC
Qy	905 ProThralaGluAsnProGluTyrLeuGlyLeuAspValProVal 919 	Qy 201 GlySerArgCysTrpGlyGluSer's

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481 FIOIIPASPG	ગ .	qq	2671 CTCGTACACAGG
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521 TrpGLyProG 	ProdlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	qa	2791 GGGGGCAAGGTG
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341 VAIGIUGIUC 	ValctucincysArgvalLeucinctyLeuProArgCintyrValAsnAlaArgHisCys 560 	qa	2851 CACCAGAGTGAT
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PRIMARY BREAST CARCINOMAS
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                                                                                                                                   OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
                   PROFILING OF PRI
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Conservative:
Mismatches:
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING
TITLE OF INVENTION: USING ARRAYS OF CANDIDAT;
FILE REFERENCE: 1546-R-00
CURRENT PAPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 3000-12-08
SOFTWARE: PATENTIN VET. 468
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 119
LEDGTH: 4530
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APPLICANT: BERTUCCI, FRANCOIS APPLICANT: BIRNBAUM, DANIEL APPLICANT: BIRNBAUM, DANIEL APPLICANT: NGUYEN, CATHERINE
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 APPLICATION NUMBER: US/10/101,510
CURRENT APPLICATION NUMBER: US/10/101,5
CURRENT FILING DATE: 2002-03-20
PRIOR PRICATION UNMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 124
LENGTH: 4530
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APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES
FILE REFERENCE: 15117.0012
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Publication No. US20030148295A1
GENERAL INFORMATION:
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                                                                                                                                                                                                   Sequence 1, Application US/10338730
| Publication No. US20030147905a1
| GENERAL INFORMATION |
| APPLICANT: Genzyme Corporation |
| APPLICANT: Genzyme Corporation |
| TITLE OF INVENTION: THERAPEUTIC COMPOUNDS |
| TITLE REFERENCE: 5017C |
| CURRENT APPLICATION NUMBER: US/10/338,730 |
| CURRENT FILING DATE: 2003-01-08 |
| PRIOR FILING DATE: 2003-01-68 |
| NUMBER OF SEQ ID NOS: 10 |
| SOFTWARE: PatentIn version 3.1 |
| SENGTH: 4530
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Indels:
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	udlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480	, da , da	261
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λ	653		653
ą	2191	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	2250
λ	653		653
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q	2851	CACCAGAGTGAGTGTGGGGGTTATGGTGTGACTGTGTGGGGAGCTGATGACTTTTGGGGCC	2910
λλ	653		653
q	2911	AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG	2970
λ.	653		653
q	2971	CTGCCCCAGCCCCCCATCTGCATGATGTCTACATGATCATGGTCAAAATGTTGGATG	3030
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λλ	654		664
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Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
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Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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Bast Jr., Robert C.
Hortobagyi, Gabriel Pusztal, Lajos
Meric, Funda
Sahin, Aysegul
Mills, Gordon B.
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Xu, Yongyao
Hoersch, Sebastian
Monahan, John
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INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
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CURRENT APPLICATION NUMBER: US/10/17,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR PLILING DATE: 2001-06-25
PRIOR PLILING DATE: 2001-06-25
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PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
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Q C	מכ	AGGACCCCCAGCCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG
oy D	665 3151	AspSerThrPheTyrArgSerLeuLeuGluAspAspAspWetGlyAspLeuValAspAla 684
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οp	3391	GCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCGAGCCAAGGGGCTGCAAAGC 3450
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APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FLING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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NAME: Sharkey, Richard G.
REGISTATION NUMBER: 32 629
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
'TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
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Patent No. 5869445
GENERAL INFORMATION:
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TITLE OF INVENTION: REAC
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TITLE OF INVENTION: ONCO
NUMBER OF SEQUENCES: 4
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CITY: Seattle
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                 GenCore version 5.1.6
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    nucleic search, using frame_plus_p2n model

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	Length: 3768 Matches: 919 Conservative: 0 Mismatches: 0 Indels: 336 Gaps: 1	US-08-625-101-1 (1-3768) MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	IleValargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	LeucysTyrClnAsyThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla [111111111111111111111111111111111111
QUENCE CHARACTERISTICS: LENGTH: 3768 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ATURE: ATURE: CDS LOCATION: 1.3765	<pre>nment Scores:</pre>) x 1 1 21 61	41 61 81 41	01 01 21 21 21 21	661 881 001 001 221 61
SEQUENCE CH LENGTH: TYPE: nu STRANDEDN TOPOLOGY: FEATURE: NAME/KEY: LOCATION: US-08-625-101-1	Alignment S. Pred. No.: Score: Percent Sim Best Local; Query Match DB:	SEQ6 (1-919, OY Db Oy Db	0y 1 0b 1 0b 1 0y 2		0

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                                                 535 GACCCGCTGAACAATACCACCCTGTCACAGGGGCCTCCCCAGGAGGCCTGCGGGAGCTG
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                                            APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
CORRESPONDENCE ADDRESS:
ADDRESSE: 10
CORRESPONDENCE ADDRESS:
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,804
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFRENCE/DOCKET NUMBER: ISIS-2913
TELECOMMUNICATION INFORMATION:
TELEFRAM: (215,568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                           Sequence 1, Application Patent No. 5968748
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                                              GENERAL INFORMATION:
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Best Local Similarity:
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TOPOLOGY: Unki
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Qy	653	653
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qq	2935	AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG 2994
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Db	3115	AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCCAGCCAG
٥y	99	AspAspMetGlyAspLeuValAspAla 684
qă	7	SCACCTICTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATG
Q <u>y</u>	80	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DÞ	3235	AGTATCTGGTACCCCAGCAGGGCTTCTTGTCCAGACCCTGCCCGGGCGCTG
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qa	3295	resticcaccacaeseacescaectical
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QQ	3355	AGGGCTGGAGCCCTCTGAAGAGGGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGG 34
Οy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGlyLeuGlnSer 764
QQ	3415	CTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGC
οy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
qa	3475	cccacacateaccccagcccrctacagcggtacagrgaggaccccacagracc
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Dp	3535	CTCTGAGACTGATGGCTACGTTGCCCCCTGACCTGCAGCCCCCAGCCTGAATATGT
δy	802	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Dp	3595	CAGCCAGATGTTCGGCCCCAGCCCCTTCGCCCCGAGAGGGCCCTCTGCCTGC
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
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		APPLICANT: RAZIUDDIN TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN TITLE OF INVENTION: NEOPLASTIC DISEASE	ESS Es	STATE: Georgia COUNTRY: usa ZIP: 30303	PE: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS	CUTRENT APPLICATION DATA: APPLICATION NUMBER: US/08/229,515A FILING DATE: 19 APR 1994	435 FORMATION: DAVID G GER: 33,4	ĭ a	Si	;		96.34% Madels: 1 Gaps:	1	21 AlaSerThrGlnValCysThrGlythrAspMetLysLeuArgLeuProAlaSerF 	41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60	61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	81 GlnGlyTyrValLeulleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 10

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	ESULT 6 S-08-645-865-9 Sequence 9, Application US/08645865 Sequent No. 5654406 GENERAL INFORMATION: APPLICANT: RAZIUDDIN APPLICANT: SARKAR, FAZLUL H TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN TITLE OF INVENTION: NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDERSS: ADDRESSERE: 127 Peachtree Street, Suite 1200	CUTY: Atlanta STATE: Georgia COUNTRY: usa CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: FILING DATE: 14 MAY 1996 CLASSIFICATION: 435	ENT FREY FOO FOO FOO FOO FOO FOO FOO FOO FOO FO	National Press 0 Length

Page 13

CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGGTT ATGCCCTATGGCTGCCTTAGACCATGTCCGGGAAAAACGGCGGACGCTGGTCCCAG	653 653 2611 GACCTGCAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2670 653	653	653	653	654	685 GlugluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704	725 LeuGlyLeuGlubroSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744 [11111111111111111111111111111111111
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Score: 4892.00 Matches: 918 Percent Similarity: 73.15% Conservative: 0 Best Local Similarity: 73.15% Mismatches: 1 Query Match: 4 Indels: 336 BB: 4 Gaps: 1 SEQ6 (1-919) x US-09-167-322-4 (1-4530)	y 1 MetGluLeuAlaAlaLeuCysAr 	Oy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40	Oy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60	61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 8 	Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100 	Qy 101 IleValargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120 	Oy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140 	Qy 141 GlnLeuargSerLeuThrGluileLeuLysGlyGlyValLeuIleGlnargAsnProGln 160 	Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180	Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200	Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrÄrgThrValCys 220	Oy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240	Oy 241 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	Oy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280 	Oy 281 SerWetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	Qy 301 TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln 320	ThralaGluAspGlyThrGlnArgCysGluLysCysSerLysP
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Page 15

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36 36 37 37	m м	<pre>Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919 lill </pre>		lanta eorgia usa 03 MABLE FORM: BP: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/(ELLING DATE: 19 APR 1994) CLASSIFICATION: 435 ATTORREY/AGENT INFORMATION NAME: PERRYMAN, DAVID G	TELECOMMENCE DOCK TELECOMMENCE 400 TELEPAN: 404 (TELEFAX: 404 (INFORMATION FOR SEE SEQUENCE CHARACT) LENGTH: 3955 I	7 Tenath	0.4420 4134.00 65.47% imilarity: 62.13% 81.41%	SEQ6 (1-919) x US-08-229-515A-14 (1-3955)

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     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                1-919) x US-08-645-865-14 (1-3955)
     9.44e-287
4134.00
65.47%
62.13%
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No.:
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oy 3 Db	320 GlnGluValThrAlaGluAspGlyThrGlnArgCysGluLySCysSerLysProCysAla 339
Oy 3 Db 10	340 ArgValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAla 359
Oy 3 Db 11	360 ASDITIEGINGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGlu 379
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0y 4	
1	26 TTCGAAACCCTGGAGGAGATCACAGGTTACCTGTACATCTCAGCATGGCCAGACACTCT 1285
Qy 4 Db 12	420 ProAspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGly 439
Oy 4	440 AlaTyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArg 459
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Oy 4 Db 14	480 ValproTrpAspGlnLeuPheArgAsnProHisGlnalaLeuLeuHisThrAlaAsnArg 499
	0 ProGludspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGly 518
-	6 CCGGAAGAGGACTTGTGCGTCTCGAGCGGCTTGGTCTGTAACTCACTGTGTGCCCACGGG 15
Qy 5 Db 15	519 HisCysTrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGln 538
Qy 5	539 GlucysvalGlucysArgvalLeuGlnClyLeuProArgGluTyrvalAsnAlaArg 558
Db 16	646 GAGTGTGTGGAGGAGTGCCGAGTATGGAAGGGCTCCCCCGGGAGTATGTGAGAAG 1705
Oy 5 Db 17	559 HisCysLeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGly 578
oy 5	598
Db 17	766 TCGGAGGCTGATCAGTGTGCAGCCTGCGCCCACTAGGACTCGTCCTCCTGTGTGGCT 1825
	ArgCysProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAsp
Db 18	826 CGCTGCCCCAGTGGTGTGAAACCGGACCTCTCCTACATGCCCATCTGGAAGTACCCGGAT 1885
Oy 6 Db 18	619 GluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAsp 638
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Db 20	2006 GAGGGCGTCCTGCTGTTCCTGATCTTAGTGGTGGTCGTTGGAATCCTAATCAAACGAAGG 2065

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2066	AGACAGAAGATCCGGAAGTATACGATGCGTAGGCTGCTGCAGGAAACTGAGTTAGTGGAG	2125
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2126	CCGCTGACGCCCAGCGAAGCCCAACCCAGCTCAGATGCGGATCCTAAAAGAGACG	2185
652		652
2186	GAGCTAAAGGAAGGTGAAGGTGCTTGGATCAGGAGCTTTTTGGCACTGTCTACAAGGGCATC	2245
652		652
2246	TGGATCCCAGATGGGGAGAATGTGAAAAATCCCCGTGGCTATCAAGGTGTTGAGAGAAAAC	2305
652		652
2306	ACATCTCCTAAAGCCAACAAAGAAATTCTAGATGAAGCGTATGTGATGGCTGGTGTGGGT	2365
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. 2366	TCTCCGTATGTGTCCCGCCTCCTGGGCATCTGCCTGACATCCACAGTACAGCTGGTGACA	2425
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2426	CAGCTTATGCCCTACGGCTGCCTTCTGGACCATGTCCGAGAACACCGAGGTCGCCTAGGC	2485
652		652
2486	TCCCAGGACCTGCTCAACTGGTGTTCAGATTGCCAAGGGGATGAGCTACCTGGAGGAC	2545
652		652
2546	GTGCGGCTTGTACACAGGGACCTGGCTGCCCGGAATGTGCTAGTCAAGAGTCCCAACCAC	2605
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2606	GTCAAGATTACAGATTTCGGGCTGGCTGGCTGGTGGACATTGATGAGACAGAGTACCAT	2665
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2666	GCAGATGGGGGCAAGGTGCCCATCAAATGGATGGCATTGGAATCTATTCTCAGACGCCGG	2725
652		652
2726	TTCACCCATCAGAGTGATGTGTGGAGCTATGGAGTGACTGTGTGGGGAGCTGATGACTTTT	2785
652		652
2786	GGGGCCAAACCTTACGATGGAATCCCAGCCCGGGAGATCCCTGATTTGCTGGAGAAGGGA	2845
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2846	GAACGCCTACCTCAGCCTCCAATCTGCACCATTGATGTCTACATGATTATGGTCAAATGT	2905
652		652
2906	TGGATGATTGACTCTGAATGTCGCCCGAGATTCCGGGAGTTGGTGTCAGAATTTTCACGT	2962
653	SerGlnAsnGluAspLeuGlyProAlaSer	662
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683	AspalaGluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGly	702
3086	GACGCTGAAGAGTATCTGGTGCCCCAGCAGGATTCTTCTCCCCGGACCCTACCCCAGGC	3145

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                                                                                                                    GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal
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                                       LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer
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2 IP: 94306

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
.*** ASSTRUCATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruegy, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory
NUMBER OF SEQUENCES: 10
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 350 Cambridge Ave. Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09146283
Patent No. 5976546
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
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REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
COUNTRY: USA
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; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
US-09-146-283-3
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Conservative:
Mismatches:
Indels:
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                                                       INFORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                      DNA (genomic)
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3632.00
98.65%
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71.52%
REFERENCE/DOCKET NUMBER:
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1751 GCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTTCCCTTCTGCGTGGCCCGCTGC
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TELEPHONE: 650-324-0880
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FINGTH: 2385 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity:
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US-08-579-823A-3
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                                                        SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene;
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Mismatches:
Indels:
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Matches:
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STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010
                                                                                                                                                                                                                                                                                                                               APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             1982 GCCGCTCGCCCAGCCCAGCACA 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 Ala --- SerProLeuAspSerThr 667
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                                                                     GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
                                                                                     IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
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120 370 140 430 160 490 180 550 200 610 220 670 240 730 260 790 280 850 300 910 320 970

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LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
                                                                   SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
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                                                                                                                                                                                                                                                                                                                                 GM-CSF-HER-2 fusion gene; Fig.
                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 INVENTION: Immunostimulatory Compositions
                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
CLASSIFICATION: <UNFORMADA
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite ?
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER:
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-344-195-3
                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-919) x US-09-344-195-3 (1-2385)
                                                                                                                                                                                                                                               NCE CHARACTERISTICS:
LENGTH: 2385 base pairs
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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3632.00
98.65%
98.65%
71.52%
TITLE OF INVENTION: IMM NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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Best Local Similarity:
Query Match:
DB:
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1391 CTGGGGAGTGGACTGGCCCTCATCC 481 ProTrpAspGlnLeupheArgAsni 1151 CCCTGGACCAGCGCCCTCATCG 501 GluAspGluCysValGlyCITTGGGAACC 501 TrpGlyProflyProTrtcllCys 1511 GAGGACGAGTGTGGGCGAGGGCC 521 TrpGlyProTrtcllCys 1511 GAGGACGAGTGTGGGCGAGGGCC 521 TrpGlyProflyProTrtcllCys 1611 [rolisginAlaLeuLeuhisThrAlaAsnArgPr 	.eualaCysHisGlnLeuCysAlaArgGlyHisCy 	/alasnCysSerGlnPheLeuArgGlyGlnGluCy 	31yLeuProArgGluTyrValAsnAlaArgH1sCy 	roGlnasnGlySerValThrCysPheGlyProGl 	iisTyrLysAspProProPheCysValAlaArgCy 	Sertyimet ProlletrpLysPheProAspGluGl 	\snCysThrHisSerCysValAspLeuAspAspLy 	SerProLeuThrSerGlnAsnGluAspLeuGlypr \GCCTCTGACGTCCCTGGAGGCACO	667 2005	JEAR LOPP)
1391 1451 1451 1511 1511 1511 1511 1511 1631 1631 16		ProTrpAspGlnLeuPheArgAsn 	GluhspGluCysValGlyGluGly/ 	TrpGlyProGlyProThrGlnCys' 	ValGluGluCysArgValLeuGlnon ValGluGluCysArgValLelllllllllllllllllllllllllllllllllll	LeuProCysHisProGluCysGln 	AlaAspGlnCysValAlaCysAla 	ProSerGlyValLysProAspLeu: 	GlyAlaCysGlnProCysProlle:	GlyCysProalaGluGlnargala: 		Pplication Hudziak, Hudziak, Hudziak, Ulbich, Ulbich, NVENTION: SEQUENCES: ES GenenteS E: Genente Outh San Fr California USA 080 EADABLE FOR TYPE: 35 15 I BM PC EADABLE FOR TYPE: 35 15 I BM PC I BM PC EADABLE FOR TYPE: 14-AF CATION DAT ION NUMBER: ATE: 11-AF CATION DAT ION NUMBER: ATE: 11-AF CATION DAT ION NUMBER: ATE: 11-AF CATION DAT ION NUMBER:
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GlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCysAla 241
                                                                                                                                                                                                                                                                                                                                                                                             182 ThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly 201
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
APPLICATION NUMBER: 08/048346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATE: 3
APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M 'REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 554C2D2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SECURED: 15/952-1994
TELECOMMUNICATION OF SECURED: 15/952-1994
TELECOMMUNICATION OF SECURED: SEQUENCE CHARACTERISTICS:
LENGTH: 1872 nuclectides
TYPE: Nucleic Acid
STRANDEDNESS: Single
15/962-983
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity:
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oy Dp	262 GIYILEÇÇSGGLULENHISGYSPROABLELENVATIRTYRASARTIRASATIRTPASTIRTPRASILUSER 281	ដ
oy Dp	282 MetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyr 301 	ದ ರ
Oy Db	pValGlySerCysThrLeuValCysProLeuHisAsnGlnGlu 3 	SS
Qy	AlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArgVal 34	
Qy	gAlaValThrSerAlaAsnIle 36	
Oy Dp	nGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPhe 381 	
Qy Db	382 AspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPheGlu 401 	
Oy Op	402 ThrLeuGluGluIleThrGlyTyrLeuTyrIleSeralaTrpProAspSerLeuProAsp 421 	
Qy Db	422 LeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAlaTyr 441 	
Qy Dp	442 SerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGluLeu 461 	
Qy Dp	462 GlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCySPheValHisThrValPro 481 	
oy B	482 TrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgProGlu 501 	
Oy Dp	502 AspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisGysTrp 521 	
çy Oğ	522 GlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCysVal 541 	
Sy GB	542 GluglucysargValLeuglnGlyLeuProArgGluTyrValAsnAlaArgHisCysLeu 561 	
Qy	562 ProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAla 581 	
Oy Dp	582 AspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCysPro 601 	

 Qy
 602 SerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGludluGly 621

 Db
 1741 AGCGGUGAAACCUGACCUCCUACAUGCCCAUCUGGAAGUUUCCAGAUGAGGACGC 1800

 Qy
 622 AlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLysGly 641

 Db
 1801 GCAUGCCACCCUUGCCCAUCACCCACUCUGGAUGACCUGGAUGACAAGGC 1860

 Qy
 642 CysProAlaGlu 645

 Db
 1861 UCCCCGCGAG 1872

Search completed: October 16, 2003, 17:20:37 Job time : 351.963 secs

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Human polynucleoti
Human HER2 (ErbB2)
Her-2/neu (ERBB2/c
Human HER2 gene.
Nucleotide sequenc
                                                                                           Human HER-2/neu on
Human HER-2/neu pr
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Human Her-2/neu CD
Human Her-2/neu CD
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HER-2 transgene pl
Human HER2 (ErbB2)
HER2 transgene pla
Sequence encoding
CDNA encoding huma
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Human tumour antig
HER-2 nucleic acid
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Human ERBB2 polynu
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Human Her2 antigen
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and is derived by analysis of the total score distribution.
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MODEL-frame+_p2n.model -DEV-x1p

-O-f-cqn_2_1/USFPO.spool_p+POLLERAM480/runat_15102003_131912_20526/app_query.fasta_1.4685
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRRNS=human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -MINLEN-0 -MAXLEN-200000000
-USER=HOLLERAN480_eCGN_1_1_1758_erunat_15102033_131912_20526 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGRPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
                                                                            October 15, 2003, 21:06:28; search time 872.869 Seconds (without alignments) 2842.104 Million cell updates/sec
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2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                        nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;

Homo sapiens

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

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01-JAN-1997 (first entry)

HER-2/neu oncogene.

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                                                                                                                                                                                                                                          Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbB2) protein (AAW01111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Ly8676-Vaal1555) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral
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is
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HER-2/neu oncogene
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Location/Qualifiers
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/*tag- /*tag- //note= "nucleotides 2026-3765 (claim 1)
HER-2/neu intracellular domain"
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malignancies with which the
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Best Local Similarity:
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654	CCTGATGGGGGGGGGGGGGGATGTTTTGGGGAATGTGGGGATGTGGGGATGTGGGGTGGGATGTGGGGTGGGATGAGGGGGTGGGATGAGGGGGTGGGATGAGGGGGTGGGTGGGTGGGATGAGGGGGG
GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG GlyMetValHisHisArgHisArgSerSerSerSerThrargSerGlyGlyGlyAspLeuThr	ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
ASPECTIFICATION OF A SECTION OF	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
1 AGGACCCCCAGCGCTTTGTGGTCATCCAGATGAGGACTTGGGCCCAGCCAG	GlyalacysGlnProCysProIleAsnCysThrHisSerCysValAspLeasAspLys 6
ATTGACTCTGAATGTCGGCCAAGATTCCGGGGGGTTGGTCTGAATTCTCCGGCATGGCC	1741 GCTGACCAGTGTGGGCCTGTGCCCACTATAAGGACCCTCCTTCTGCGTGGCCGCGTGC 1800 601 ProSerGlyValLySProAspLeuSerTyTMetProIleTrpLySPheProAspGluGlu 620 111111111111111111111111111111111111
1 AAACCTTACGATGGGATCCCAGCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG	561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
653	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGGCGGCGGTTCACC	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
653 653 2581 ATTACAGACTTCGGGCTGGCTGGCTGGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2649	501 GluaspglucysvalGlyGluGlyLeualaCysHisGlnLeuCysalaArgGlyHisCys 520
31 1 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA	481 ProtrpaspGlnLeuPheargasnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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Best Local Similarity:
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                                   This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing
TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr
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/note= "region which elicits immune response"
                                                                       905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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/product= "HER-2/neu"
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Conservative:

Length: Matches:

6.12e-227 4900.00 73.23%

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Pred. No.:

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                    LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu
                                                                             ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal
                                                                                                         AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla
                                                                                                                                       ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal
                                                                                                                                                                                             GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu
                                                                                                                                                                                                                                                                                                                                                     Antigen-presenting cell; immunogenic; immune response; HBR-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
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/product= "HER-2/neu protein"
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P-PSDB; AAB85458.
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GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys

AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu

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21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu

1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla

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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antignen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, or so breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/neu protein (also known as pl85 or c-erbB2).
                 New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
                                                                                                                                                                                                                                                                                                                                                                Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
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Mismatches:
Indels:
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                         2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC
                                     ------GlnAsnGluAspLeuGlyProAlaSerProLeu
                                                                                      GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
                                                                                                                GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr,
                                                                                                                                        LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly
                                                                                                                                                                AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer
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effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HiA)-144 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a chuman patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centire Her-2/Neu gene for making the direct expression of a collypeptide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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dene;
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human leukocyte antigen; HLA; vaccine; malignancy; cytostatic;
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Mcneill PD, Vedvick TS;
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P-PSDB; AAE20479.
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ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLe	GluLeuThrTyrLd GAACTCACCTACC	GINGlyTyrValLeuIlealaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	IlevalargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 	ASPProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 	GINLeuargSerLeuthrGluileLeuLysGlyGlyValLeuileGlnargAsnProGln 	. LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 	1 LeuThrLeuIleaspThrasnargSerargAlaCysHisProCysSerProMetCysLys 	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 	AladiydiycysAlaargcysLysGlyProLeuProThrAspcysCysHisGluGlnCys	AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 	TyrasntyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisAsnGln 	GluvalThralaGluaspGlyThrGlnArgCysGluLysCysGruLysCysBroCysAlaarg 	ValcystyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 	IleGInGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 	PheAspGlyAspFroAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
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οχ	401	TreuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpFroAspSerLeuPr
qa	1201	GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT
Οy	421	spLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAl
qa	1261	GAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGC
Οy	441	TLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuAr
Db	1321	ACTCGCTGACCCTGCTGCTGGCTGGCTGGCTGGGCTGGG
οy	461	uGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHis
Dβ	1381	CAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGT
Qy	481	roTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPr
Db	1441	GGGACCAGCTCTTTCGGAACCCGCAC
٥y	501	GluAspGluCysValGlyGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
QQ	1501	GGACGAGTGTGTGGGCGGGGCCTGGCCTGCCACCTGTGCGCCCGAGGGCACTG
Οy	521	rpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCy
QQ	1561	GGTCCAGGGCCCACCCAGTGTTTTTTTTTTTTTTTTTTT
٥y	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Dp	1621	GAGGAATGCCGAGTACTGCAGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTG
οy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db	1681	SCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGA
οy	581	pGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCy
Db	1741	
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
QQ	1801	CAGGGGGGGTGTGAAACCTGACTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGA
٥y	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db	1861	GGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGGACCTGGATGACAA
ΟY	641	lyCysProAlaGluGlnArgAlaSerProLeuThrSe
Db	1921	CTGCCCCGCCGAGCAGAGCCAGCCCTCTGACG
Qy	653	
Db	1981	ATTCTGCTGGTCGTGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040
Οy	653	
Db	2041	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
οy	653	653
Db	2101	ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160
ΟY	653	653
Db	2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
Qy	653	653
Db	2221	CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280

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VallysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
CCCTCTGAGACTGATGGCTACGTTGCCCCCCTGACCTGCAGCCCCAGCCTGAATATGTG
                        AsnGlnProAspValArgProGlnProProSerProArgGluG1yProLeuProAlaAla
                                         GGAGGAGCTGCCCCTCAGCCCCACCTCCTCCTGCCTTCAGCCCTTCGACAACCTC
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P-PSDB; AAM51143.
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904 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr The present sequence is that of human Her-2/neu oncogene cDNA. The cDNA encodes Her-2/neu (p185), an oncogenic self protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kiṇase; receptor; human; gene therapy; gene; ss.

ovarian, colon, lung and prostate cancer. Her-2/new is a member of the tyrosine kinase family of receptor-like glycoproteins. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/new fusion proteins proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/new protein is fused to a Her-2/new intracellular domain or phosphorylatin domain (or its Deltapb fragment). An immune response to Her-2/new protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion proteins, nucleic acids, and isolated content in the fusion proteins, nucleic acids, and isolated content in the development of a necessial for inhibiting the development of a necessial for the animal the fusion proteins of the necessial for inhibiting the development of a necessial for the animal the fusion proteins of the necessial for inhibiting the development of a necessial for the animal the fusion fusion for a necessial for inhibiting the development of a necessial for the animal the fusion for a necessial for inhibiting the development of a necessial for the animal the fusion for a necessial for inhibiting the development of a necessial for the animal the fusion for a necessial for inhibiting the development of a necessial for the animal the fusion for a nec cancers, including breast, cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in a sample to inhibit the development of cancer in a patient. BP; 759 A; 1171 C; 1119 G; 719 T; 0 other; 3768 919 0 0 336 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: of overexpressed in a variety 6.12e-227 4900.00 73.23% 73.23% 96.49% Percent Similarity: Best Local Similarity: Sequence 3768 Alignment Scores Pred. No.: p185 Best Local Si Query Match: DB: order Score:

SEQ6 (1-919) x ABA92250 (1-3768)

1020 1080 1140 1200 1260 1320 1620 1680 1500 1560 340 360 380 440 240 780 280 840 300 320 960 400 420 260 220 999 720 260 900 480 500 520 540 580 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 961 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA GGCTCCCGCTGCTGGGGGGGGTTCTGAGGATTGTCAGAGCCTGACGCGCACTGTCTG AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis ValCysTyrGlyLeuGlyMetGluHisLeuArqGluValArqAlaValThrSerAlaAsn GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu GlySerArqCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArqThrValCys PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe LeuGlySerGlyLeuAlaLeuIleHisHisHsnThrHisLeuCysPheValHisThrVal CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCACACGGTG ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 1021 1141 841 901 361 1081 1321 1381 1501 241 781 281 301 341 381 1201 1261 441 1561 1621 201 601 221 661 721 261 321 401 421 481 501 521 541 561 461 g ò Q δŽ g δ g οy qq δ qq οy Q ŏ g ŏ g οy qq ŏ qq δ qq ò g qq ò ŏ qq δ Q δ Dp δ QQ ŏ

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                                                                                                                                                                                                                                                                                                                             Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the
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                   Human; Her-2/neu; gene; ds; cytostatic; haematological malignancy; CM acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL; chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS; Hodgkin's lymphoma; T cell therapy.
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q	CTGGCTCCGAT	GTATTTGATGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCAAA
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                  GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu
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                                                                                                                                   TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr
                                                                                                                                             The present sequence encodes a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating damaged cells including conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                           SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
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ErbB-2;
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This invention describes a novel method for generating a cellular immune response in a patient to a target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. cancerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents a DNA fragment which encodes the human tumour antigen ErbB-2 described in the method of the
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                                                                                   comprises introducing vector with nucleotide sequence encoding immunogen comprising protein processing signal into cell of patient
                                                                                                                                                                                                                                                                                                                                                   disclosed
                                                                      cellular immune response in patient to target protein
                                                                                                                                                                                                                                                                                                                                                  information in this spec has been previously disclosed the however this spec contained no sequence information
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                                                                HER-2; c-neu; ErbB2; transmembrane receptor; tyrosine kinase activity; epidermal growth factor receptor; EGFR; HER-1; cancer; breast cancer; ovarian cancer; gastric cancer; antisense oligonucleotide; expression; hyperproliferative disease; ss.
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414	. Q . W	140 594	160 654	180	200	220 834	240 894	260 954	280 1014	300 1074	320 1134	340 1194	360 1254	380 1314	400	420	440
	IleValargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGl 	AspproLeuAsnAsnIhrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 	1 GlnLeuargSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	1 LeucysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	1 LeuThrleulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysTys	1 GlyserargcysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 	1 AladlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGludlnCys	AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 	1 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	1 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	GluvalThralaGluaspGlyThrGlnargCysGluLysCysSerLysProCysAlaarg 	1 ValcysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 	1 IleGlnGluPheAlaGlyCysLysLysLlePheGlySerLeuAlaPheLeuProGluSer 	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	1 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArglleLeuHisAsnGlyAla
355 81 815	0 7	121	141	161	181	201 775	221	241	261 955	281	301	321	341	361 1255	381 1315	401	421
4 6 A	Qy	Qy Db	Qy	QY Db	QY Db	Qy Db	Oy Db	Qy	Qy	Qy	Qy	Qy	Qy	Qy	Qy	Qy	Qy

1734 2154 1435 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCC 1494 1554 1614 520 540 1794 560 1854 1914 1974 2034 2214 2274 2334 2394 2514 480 500 2515 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACATT 2574 580 009 620 653 653 653 653 653 653 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 2095 GGCTGCCCCGCCGAGAGAGACCACCACCTCTGACGTCCATCATCTCTGCGGTGGTTGGC 2275 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2335 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2395 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 2155 ATTCTGCTGGTGGTCTTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2215 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer------441 461 1555 481 1615 1675 521 1735 541 561 653 653 653 2455 653 653 653 653 g Dp g g òγ g QΥ g Qγ d $\delta \lambda$ a Q Qγ g δý Db g οy qq δλ g P δλ δý ŏλ δ Q δ Ω g ÓΣ g qq

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0у 65	53 653
Db 257	75 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2634
Qy 65:	53 653
Db 263	35 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694
oy 65	53 653
Db 269	95 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2754
oy 65	53 653
Db 27!	55 ATTACAGACTTCGGGCTGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2814
oy 65	53 653
Db 281	15 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGGCGGCGGTTCACC 2874
2y 6!	53 653
Db 287	75 CACCAGAGTGATGTGTGGAGTTATGGTGTGTGTGTGGGGGGCTGATGACTTTTGGGGCC 2934
Dy 65	53 653
Db 293	35 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG 2994
оу 6	53 653
Dp 299	95 CTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3054
Qy 65	53 653
305 a05	55 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 3114
0y 65	54
Db 311	5
оу 66	65 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
317	Ŋ
0y 6E	85 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 323	35 GAGGAGTATCTGGTACCCCAGCAGGCCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG 3294
0y 70	05 GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 329	LO.
7	25 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 335	55 CTAGGGCTGGAGCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGG 3414
0y 74	15 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGlyLeuGlnSer 764
Db 341	5 GCTGGCTCCGATGTATTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGGCTGCAAAG
0y 76	65 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 347	'n
Qy 78!	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVa
Db 353	CCCTCTGAGACTGATGGCTACGTTGCCCCCCTGACCTGCAGCCCC
Qy 80	35 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
355 qa	

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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary artery endothellum, umbilical artery or vein endothellum, coronary artery andothellum, umbilical artery or vein endothellum, coronary artery andothellum, pulmonary artery conditions and microvascular endothellum, pulmonary artery conditions. The part of pathellum, pronchial epithellum, mammary epithellum, prostate epithellum, renal cortical epithellum, renal proximal tubule epithellum, combilical artery smooth muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, pulmonary artery smooth muscle, coronary artery smooth muscle, mesangial cells, coronary artery smooth muscle, coronary artery arte
3775 GGAGGAGCTGCCCTCAGCCCCACCTCCTCCTGCTTCAGCCCAGCCTTCGACACCTC 3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3835 TATTACTGGGACCAGGACCCACCAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGGACA 3894
                                                                                                                                                                                                                                                                                                                             3715 GTCAAAGACGTTTTTGCCTTTGGGGGTGCCGTGGAGAACCCCGAGTACTTGACACCCCAG 3774
                                                                                                                                                                                                                            864
                                                                                                                                                                                                                                                                                                                                                                                                                                              884
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bronchial epithellum; prostate; muscle; lung fibroblast; osteoblast;
tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
gene expression; gene; ss.
                                                                                                                                                                                                                       845 ValLysAspvalPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                              865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene expression profile polynucleotide SEQ ID NO 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ34969 standard; cDNA; 4473 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2003 (first entry)
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involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein
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888888	expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents.	
S S	173 BP; 902 A; 1383 C; 1329 G	
Align Pred Score Perce Best Query DB:	Jument Scores: 7.31e-227 Length: 4473 1. No.: 4900.00 Matches: 919 2. Sont Similarity: 73.23% Conservative: 0 2. Local Similarity: 73.23% Mismatches: 0 2. Indels: 336 2. Gaps: 1	
SEQ6	6 (1-919) x ABZ34969 (1-4473)	
οy	CysArgTrpGlyLeuLeuLeuAlaLeuLeuProFroGlyAla	20
qq	SAAGCTGGCGGCCTTGTGCCGCTGGGGGCTCCTCGCCCTCTTGCCCCCC	234
δō i	21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	0
ga .	S GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGTCCCTGCCAGTCCCGAG	
Š Š	4.1 ThrHisLeuAspWetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 	0 1
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δδ.	61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspileGlnGluVal	0
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7 A		i m
٥y	SerProGlyGlyLeuArgGluLeu	140
qq	535 GACCCGCTGAACAACCCCCTGTCAACGGGCCTCCCCAGGAGGCCTGCGGGAGCTG 5	594
δλ	141 GInLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	160
qq	AGCTICGAAGCCICACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	654
δλ	161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
QQ	TCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCT	714
Qγ	181 LeuThrLeulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 2	200
qq	CTCTCGGGCCTGCCACCCTGTTCTCCGATGTGTAAG	774
Oy	201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 2	220
qq	ccecrecresesasasaricresesariercasascresesescreterer	834
δλ	221 AlaGlyGlyClyCysAlaArgCysLySGlyProLeuProThrAspCysCysHisGluGlnCys 2	240
qq	GGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT	894
Οy	laalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
q	creccrecracracaaccac	954

Qy	261	lleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
QQ	955	GIGGCATCTGTGAGCTGCTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAG
δy	281	TWETProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
qa	1015	CGGTATACATTCGCCGCCAGCTGTGTGTGTGTCGCTGTCCC
Οy	301	rAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAs
qa	1075	ACAACTITCTACGGACGTGGGATCCTGCACCTCGTCGCCCCGTGCAACCAA
Qy	321	ValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
qa	1135	AGGTGACACAGAGGATGGAACACAGGGTGTGAGAAGTGCAGCAAGCCTGTGCCCGA
Qy	341	CysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn
qa	1195	TGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGTGAGGTAACCAGTGCCAAT
Qy	361	eGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheEeuProGluSer
qa	1255	CAGGAGTTTGCTGGCTGCCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGGAGAGC
QY	381	eAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
qa	1315	GGGACCCAGCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT
Qy	401	1ThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro
qa	1375	SATCTCAGCATGCCGGACAGCCTGCCT
Qy	421	oleuSerValPheGlnAsnLeuGlnValIleArgGlyArglleLeuHisAsnGlyAla
QQ	1435	GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCC 1494
QY	441	SerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu
qa	1495	ACTGAGGGAA
Qy	461	IGLYSerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
qa	1555	GGCAGTGGACTGGCCCTCATCCACCATAAACACCCTCTGCTTCGTGCACCGTG
Qy	481	OTTPASPGInLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
Ор	1615	CCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCTGCTCCACACTGCCAACCCGCCA
Qy	501	nAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
qa	1675	GAGGACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy	521	y61yPro61yProThrGlnCysValAsnCysSerGlnPheLeuArgĠlyGlnGluCys
qa	1735	GGGGTCCAGGGCCCACAGTGTGTTTTTTTTTTTTTTTTT
Qy	541	alGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
qa	1795	STGAATGCCAGGCACTGT
Qy	561	uProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
qa	1855	TGCCGTGCCACCCTGAGTGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG
Qy	581	aAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
qa	1915	GACCAGTGTTGTGTGTGTGTGTGTTATAAGGACCCTCCCT
QY	601	SerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu
qa	1975	CCAGCGGTGTGTAAACCTGACCTCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG
Oy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640

5 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	31/3 GACACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3234 685 GluGluTyrLeuValProGlnGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704	3235 GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG 3294	GlymetvalHisHisArgHisArgSerSerSerTergSerGlyGlyGlyAspLeuThr	5 GGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGACCTGACA	725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744 	ען שפרטי מפרטי פרטי פרטי פרטי פרטי פרטי פרטי פרטי	/43 AtacutySertabratraspelyAsapleduciyMetotyAtachariaySelyPeducibatra 	765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784	3475 CTCCCCACACATGACCCCAGCCCTACAGGGGTACAGTGAGGACCCCACAGATACCCCTG 3534	5 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	S CCCTCTGAGACTGATGGCTACGTTGCCCCCTGACCTGCAGCCCCCAGCCTGAATATGTG		333 AACCAGCAGATGTTCGGCCCCAGCCCCCTCTGAGAGGCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal	5 CGACCTGCTGGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCCAGGGAAGAATGGGGTC	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	5 GTCAAAGACGTTTTTGCCCTTTGGGGGGGCCCGGAGACCCCGGGGTACTTGACACCCCGG	805 GIVGIVALAATAPTOGINFYOHISPYOPYOPYOALAPNESSEYPOALAPNEASSASTNEN 884	5 Terminimatendi nasabinatandi liberadi ishababindan darihat bali waki	35 TATTACTGGGACCAGGACCCACCAGGGGGGGGCTCCACCACCAGGACCTTCAAAGGGACA	905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919	3895 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3939	11 4	AAD38904 standard; DNA; 4473 BP.	D38904;	-SEP-2002	man Her-2 DNA.	<pre>man; Her-2; epidermal growth factor receptor 2; infect perproliferative disorder; prophylaxis; inflammation;</pre>	tumour; gene therapy; phosphorothioate backbone; gene; ss.	mo sapiens.	Key Location/Qualithers CDS 1753942 /*tag= a
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Db 2035 GGCGCATGCCCCATCACCTGCACCCACTCCTGTGTGGACCTGGATGACAAG 2094 Oy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	rrege 21	2		Db 2215 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2274	Фу 653 653	Db 2275 ACACCTAGCGGAGCGATGCCCAACCAGGGGGGATGCGGAAAGAGAGGGGGGGG			Db 2395 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2454	65	Db 2455 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGGGCTCCCCA 2514	Фу 653 653	Db 2515 TATGTCTCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACTT 2574	Ογ 653 653	Db 2575 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2634	Ογ 653 653	Db 2635 GACCTGCTGAACTGGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694	Оу 653 653	Db 2695 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2754	653	DD Z/33 ATTACAGACTICGGCTGCTGCTGGGACATTGACGAGAGAGAGGAGGAGAGTACCATGCAGGT Z814	7		Db 2875 CACCAGAGTGTGTGGGGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2934	Оу 653 653	Db 2935 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGGAAAAGGGGGAAGCGG 2994	Qy 653 653	Db 2995 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3054	Oy 653 653	Db 3055 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGGAATTCTCCCGCATGGCC 3114	Qy 654

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                                                                                                                                                                                Human
                                                                                                                                                                                                                                        The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. Lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
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  Her-2
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55 ATTACAGACTTCGGGCTGGCTGGCTGGTGGACATTGACGAGACAGAC	653	654		745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGlyLeuGlnSer 764	1	55 CGACCTGCTGCTGCACTCTGGAAAGGCCCAAGACTCTCCCCCAGGGAAGAATGGGGTC 56 CGACCTGCTGCTGCACACTCTGGAAAGGCCCCAAGACTCTCTCCCCCAGGGAAGAATGGGGTC 57 CGACCTGCTGCTGCAAAGGCCCCAAGACTCTCTCCCCCAGGGAAGAATGGGGTC 58 CAAAAGACGTTTTTGCCTTTGGGGGTGCCGTGGAAAACCCCCGAGTACTTGACACCCCCAG 59 CAAAAGACGTTTTTGCCTTTGGGGGTGCCGTGGAAAACCCCCGAGTACTTGACACCCCCAG 56 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520 1675 GAGGACGAGTGTGGGCGGGCCTGCCAGCAGCTGTGCGCCCGAGGGCACTGC 1734 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 1735 TGGGGTCCAGGCCCACCCAGTGTCAACTGCAGCAGTTCCTTCGGGCCAGGAGTGC 1794 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyTValAsnAlaArgHisCys 560 1795 GTGGAGTATGCAGGGCCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT 1854	561 LeuProCysHisProGlucysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580	1 GlyalacysGlnProCysProlleAsnCysThrHisSerCysValaspleuAspAspLys 1 GlyalacysGlnProCysProlleAsnCysThrHisSerCysValaspLeuAspAspLys 1 Hillillillillillillillillillillillillill	653 653 2155 ATTCTGCTGGTCGTCGTCGTCGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2214 653 653 2215 AAGATCCGGAAGTACACGATGCGGAGATGCTGCAGAAACGGAGCTGGTGGAGCCGCTG 2274 653 653 2275 ACACCTAGCGGAGCGATGCCCAACCAAGCGGATCCTGAAAGAGAAGAAGAAAGA	3	653	653
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The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human crostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or ibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (I) at least 1 CTL (cytotoxic T-lymphocyte) croup derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used the respective PA and including at least one foreign T helper epitopes of the respective PA and including at least one foreign T helper epitopes of the respective PA and including at least one foreign T helper between are also claimed. The method is used the respective PA and including at least method is used the respective pare and an and an analogue of the respective PA and including at least one foreign to the PA is human pare the pare are also claimed.
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                                                                                                                                                                                                                                                                                        Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing immune responses to weakly immunogenic, tumor associate peptide antigens for the treatment of breast and prostate cancer
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                                 T; 0 other;
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      GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspileGlnGluVal
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	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 5	QG q	1 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA
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		qa	2581 ATTACAGACTTCGGGCTGGCTGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 5	Oy	653 653
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	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560	δ d	
	1621 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT 1680	a :	2/01 CACCAGAGIGAIGIGIGIGIGAGITAIGGIGIGACTGIGIGGGAGCTGATGACTTTTGGGGCC 2/60
	561 LeuproCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 1 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1	S 6	1 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG
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	ProSerglyValLysProAspleuSerTyrWetProIleTroLysPheproAspGluglu	ογ	653 653
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	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	Qy Db	654
	1801 GGCGCATGCCAGCCTTGCCCATCACTGCACCCACTCCTGTGGACCTGGATGACAG 1920 641 GlyCysproblagluGlobralaSarbrofoumhrear	Oy	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
	647-77-77-77-77-77-77-77-77-77-77-77-77-7	qq	3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT 3060
		٥y	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
	1981 ATTCTGCTGGTCGTCGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCAGCAG 2040	qa —	1 GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG 3
	653 653	δ O	GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyGlyBibrr
	2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2100	qq	21 GGCATGGTCCACCACAGGACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGACCTGACA 3
	653 653	λo d	/25 LeuGlyLeuGluProSerGluGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160	g :	CIANGGUIGGAGUCCITIGAAAGAGAGGCCCCCCAGGITTCCACIGGCACCCITCCGAAGGG 3/4
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	2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	3 —	לאיד. סליו מסליו לכנסחו מיחודו מחומפו סחלכו ומסקמחו מסקפט החכלה חכלה מליח מליח מליח מליח מליח מליח מליח מליח

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                                                                                                                           864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonuclectides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each
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                                                                                                                                                                                                                                                                                                                                 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HTV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating tumors,
that are
                                                                                                                                                                                        ArgProalaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal
                                                                                                    LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu
                               ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal
                                                               AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla
                                                                       ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           introducing into
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of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the
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QY	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280	6y 6y	621 GlyAlaCysGlnProCy
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Qy	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	λ (c)	041 GIYCYSPIOAIAGIUGI
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6	341 VALCYSIY.toly.teUolymeUolumisheuargoluValatgalaValiniseRalaash 360 	q _Q	2101 ACACCTAGCGGAGCGAT
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: 음		qq	2161 AGGAAGGTGAAGGTGCT
ò	lnValPhe 40	Qy	653
- q	1141 TTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGAGCAGCTCCAAGTGTTT 1200	qa	2221 CCTGATGGGGAGAATGT
OX	4	Qy	653
. qa		Dp	2281 CCCAAAGCCAACAAAGA
Qy	421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440	Qy	3
qq	1261 GACCTCAGCGTCTTCCAGAACCTGCAGTAATCCGGGGACGAATTCTGCACAATGGCGCC 1320	qa —	2341 TATGTCTCCCGCCTTCT
Οy	441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	oy	
qo	1321 TACTCGCTGACCCTGCAAGGCTGGGCATCACCTGGGGCTGGGGCTGCGCTCACTGAGGAA 1380	<u>a</u>	Z4Ul ATGCCCTATGGCTGCCT
δλ	461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480	δŏ	
g	1381 CIGGGCAGTGGCCCTCATCCACCATAACACCCACTCTGCTTCGTGCACACGGTG 1440	qu	6:1 GA(
٥y	pAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArg	Oy	
Dp	1441 CCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACCTGCCAACCGGCCA 1500	q 0	$^{\circ}$
Qy	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	Oy	
qq		qq	2581 ATTACAGACTTCGGGCT
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7 A		qu	2641 GGGGGCAAGGTGCCCAT
è	ValginginovsArgValiengingivienDroArgGinTvrValasnalaargus 560	Oy.	653
; f		qa	2701 CACCAGAGTGATGTGTG
l ò	LeuProCvsHisProGluCvsGloProGluAsnGlvSerValThrCvspheGlvProGlu 580	Qy	653
. a	TTGCCGTGCCACCCTGAGTGCCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 1	qa	2761 AAACCTTACGATGGGAT
Qy	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	Qy	
qq	1741 GCTGACCAGTGTGGCCCTGTGCCCACTATAAGGACCCTCCCT	q °	2821 CTGCCCCAGCCCCCAT
Qy	601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620	δō	
		qa	2881 ATTGACTCTGAATGTCG

STCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGCTCCCAG 2460 CTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860 CGATGCGGAGACTGCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2100 VIGCCCAACCAGGCGCAGAIGCGGAICCTGAAAGAGACGGAGCIG 2160 TTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220 TGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280 MANATCTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA 2340 TIGGGCATCTGCCTGACATCCACGGTGCAGCTGACACAGCTT 2400 GTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520 FIGGCICGGCIGCIGGACATIGACGAGACAGAGTACCAIGCAGAI 2640 GGAGTTATGGTGTGTGTGTGTGGGAGCTGATGACTTTTGGGGCC 2760 JTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040 TGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580 VICTGCACCATTGATGICTACATGATCATGGTCAAATGTTGGATG 2880 IGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 2940 VICAAGIGGAIGGCGCIGGAGICCATICICCGCCGGCGGTICACC 2700 653 653 653 653 653 653 653 653 653 653 .----- 653 *************************

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                                                                GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
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               AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla
                                                                                 GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG
                                                                                                                                  LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly
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                                                                                                 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr
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241 CAGGGCTACGTGCTCATCGCTCACAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGG

GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg

IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly

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target gene by introducing into the cell that contains the target gene target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsnal) that has a double stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon Defore introduction of dsnNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) control genes, particularly oncogenes, cytokine genes, Id (not defined) control genes, and genes, and genes expressed in pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsnNA can inhibit expression of the target genes, and the effect is even greater when dsnNA are modified to increase their stability. ABX09936-ABX10075 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon
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2520	1 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG	246
653	3	65
2460	1 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG	240
653	3	9
2400	1 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTG	234
653	3	65
2340	1 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCC	228
653		65
2280	1 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACAC	222
653	33	<u> </u>
2220	1 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTTGGCACAGTCTACAAG	216
653	33	65
2160	1 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCT	210
653	33	65
2100	1 AAGATCCGGAAGTAC	204
653	33	65
2040	1 ATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAA	198
653	3	65
1980	1 GGCTGCCCGCCGAGCAGAGCCTCTCTCTCTCTCTCTCTCT	192
1920	1 GGGGCATGCCATGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAA	186
640	1 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysV	62
ı co	1 CCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGG	
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600	1 AlaAspClnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	58 174
1740	1 TTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGAGCTGTTTTGGACCGGGAG	168
280	1 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProC	95
560	1 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 	54
540 1620	1 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	52 156
520 1560	1 GluaspGluCysValGlyGluGlyLeualaCysHisGlnLeuCysAlaArgGlyHisCys	50

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SEQ6 (1-919) x AAD43935 (1-3768)
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The invention relates to a transgenic non-human mammal that produces in its mammary gland cells detectable levels of a native human HER2 protein or its fragment. The transgenic animals are useful as tumour models for testing HER2-directed cancer therapies, and for identifying anticancer agents. The animals may also be used as source of cells which can be immortalised in culture, in screening for compounds that have potential as prophylactic or therapeutic treatments of diseases or disorders involving expression of HER2. The anti-cancer molecules are useful for inducing apoptosis or cell death of cancer cells. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic non-human mammal that produces detectable levels of a native human HER2 protein in its mammary gland cells, useful as tumor models for testing HER2-directed cancer therapies, and for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                   tumour;
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MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 	AlaSerThrGlnValCysThrGlyThrAspWetLysLeuArgLeuProAlaSerProGlu 	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 	GINGLYTYTVAILeuIleAlaHisAsnGINVAlArgGINVAIPTOLeuGINArGLEUARG 	IlevalArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 	AspProteuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 	GINLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 	LeuThrLeuIleaspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn
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-MODEL=frame+_p3n.model_-DEV=xlp
-MODEL=frame+_p3n.model_-DEV=xlp
-G-/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_15102003_131912_20536/app_query.fasta_1.4685
-DB-GenEmb1_-OFMT=fastap -SUFFIX=rge -MINAMTCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN-200 -THR_SCORE=pct -THR_MAX=100 -THR_MNN=0 -ALIGN-15 -MODE-LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLENG - MAXINEN=2000000000
-USER=HOLLERAN480_CGCN_1_1_22724_Grunat_15102003_131912_20536 -NCPU=6 -ICPU=3
-NO_MMAP = LARGEQUERY -NEG_SCORESO -MATRIX=DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARR_TIMEDOT=30 -THREADS=1 -XCAPOP=10 -XGAPOF=6.5 -FGAPOP=6
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nA eactiv	 		uLeuA CCTCG	steuA 	yCysG CTGCC	rPheL	9G1nV	rAlar IIII	aSerP	yvall 	ePheH 	SHisP CCACC	sglns TCAGA
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AR034479 Sequence 1 from patent US 586944 AR034479 AR034479.1 GI:5950084 Unknown. M Unknown. Unclassified. 1 (bases 1 to 3768) Cheever,M.A. and Disls,M.L. Methods for eliciting or enhanci Patent: US 5869445-A 1 09-FEB-12 Location/Qualifiers ce /organism="unknown" T 759 a 1171 c 1119 g 7	ores: larit imila	x ARO	1 Met	21 Ala 61 GCG	41 Thr 21 ACC	61 Glv 81 GAA							
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ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu TTGCCGTGCCACCCTGAGTGTCAGCCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro qq οχ 염 δ Db δ Q gg οy QQ ΟY 0y 0b δ g o Db Qy QQ οy g οy g ò g ζ g ò g ò g δ D à

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8 &	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160 653	ολ	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer
q	2161 AGGAAGGTGAAGGTGCTTCGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	ਰ ਹ	GCTGGCTCCGATGTATTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCAAAGC 3
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අු	2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280	δŏ	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal
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7 A	TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT	qa	3421 AACCAGCAGATGTTCGGCCCCCAGCCCCTCTGCCCCAGAGGGCCCTCTGCTGCTGCC 3480
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qa	2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460	g :	1 CGACCTGGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGTC 3
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අ :	2461 GACCTGCTGAACTGGTGTATGCAGAATTGCCAAGGGATGAGCTACCTGGAGGATGTGGGG 2520	δλ	GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 8
S 8	2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580	qu	3601 GGAGGAGCTGCCCTCAGCCCCACCCTCCTGCCTTCAGCCCAGCCTTCGACAACCTC 3660
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q	2701 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760	DEFINITION	AAZULO1/ Sequence 1 from Patent WO0153463.
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Cheever, M.A. and Hand-Zimmermann, S. Compounds and methods for prevention and associated malignancies Patent: WO 0153463-A 1 26-JUL-2001; CORIXA CORPORATION (US)
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                                                                   LeuCysTyrGlnAspThrlleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla
                                                                                                                                                          SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
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	Qy	1	MetGluLeuAlaAlaLe	uCysAr	gTrpGlyLeuLeuLeuAla	laLeuLeuProProGlyAla	20
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	ΟY	21	AlaSerThr	erThrGlnValCysThrGlyThrAs	hrAspMetLysLeuArgL	rgLeuProAlaSerProGlu	4.0
	qq	61	- ~	CAAGTGTGCACCGGCAC	- 6	TCCCTGCCAGTCCCGAG	120
	Qy		ThrHisLeu?	uAspMetLeuArgHisLeuT	euTyrGlnGlyCysGlnValVal	GlnGlyAsnLeu	09
_	qa	121	Ç	sacarecreeceace	rcraccagggcrgccz	CAGGGAAACCTG	180
	Οy	61	luLeuThr	TyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAs	laSerLeuSerPheLe	pileGlnGluVal	80
	qq	181	GAACTCACCT	raccreccaccaare	ccaeccrerccrrccr	TATCCAGGAGGTG	240
	Qy	81	GlnGlyTyrV	yrValLeuIleAlaHisAs	HisAsnGlnValArgGlnVa	alProteuGlnArgLeuArg	100
	Op Op	241	AGGGCT	srecrearcecreaca.	ACCAAGTGAGGCAGGT	ccacrecagasecrece	300
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	αn	301	TTGTGCGA	sgcacccagcircirirg#	AGGACAACTATGCCC		360
	Qy	121	SpPro		1ThrGlyAla	SerProGlyGlyLeuArgGluLeu	140
	ρp	361	S	CCACCCTG	rcacaggggc	TGCGGGAGCTG	420
	Οy	141	InLe	uArgSerLeuThrGluIleLeuLysGlyGlyVa	euLysGlyGlyValLe		160
	Dβ	421	SCT	AGCCTCACAGAGATCTT	rgaaaggaggggrctr	cagoggaaccccag	480
	٥y	161	euCy	SlnAspThrIleLeuTr	rpLysAspIlePheHi	sTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla	180
	Ωp	481		CAGGACACGATTTTGTC	SGAAGGACATCTTCC	- =-	540
	Οy	181	euT	hrLeuIleAspThrAsnArgSe	erArgAlaCysHisProC	ysSerProMetCysLys	200
	qq	541	CTCACACTGA		cressecreceace	GTTCTCCGATGTGTAAG	009
	Qy	201	GlySerArgC	CysTrpGlyGluSerSerG	luAspCysGlnS	rLeuThrArgThrValCys	220
	pp	601	TCCCGC	CTGGGG	AGGATTGTCAGA	ccreacececrererer	099
	Qy	221	AlaGlyGlyC	.yCysAlaArgCysLysGlyF	I	spCysCysHisGluGlnCys	240
	QQ	661	GTGG	SCCCCCTC	SGCCACTGCCCACTG	TGCTGCCATGAGCAGTGT	720
	Qy	241	laAlaGl	yCysThrGlyProLysHi	ProLysHisSerAspCysLeuAlaCysLeuHis	PheAsnHis	260
	Db	721	95556	SACGGGC	ACTCTGACTGCCTGG	TTCAACCAC	780
	Qy	261	erGlyIl	eCysGluLeuHisCysProAlaLeuVa	roAlaLeuValThrTy	alThrTyrAsnThrAspThrPheGlu	280
	Db	781	SGCAT	rereactect	CAGCCCTGGTCACCTA	ACGTTTGAG	840
	٥y	281	erMetPr	OASnProGluGlyArgTy	yrThrPheGlyAlaSerCy	srCysValThrAlaCysPro	300
	qq	841	CATGCC	rcccaaggccggr	ATACATTCGGCGCCAG	rgreacrecter	006
	Οy	301	yrAsnTy	rLeuSerThrAspValGlySerC	ySerCysThrLeuValCys	ProLeuHisAsnGln	320
	Db	901	Ē	CTACGG	SATCCTGCACCCTCG	ccccrecaccaa	096
_	Οy	321	GluValThrAl	AlaGluAspGlyThrGl	lnArgCysGluLysCy.	sSerLysProCysAlaArg	340

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RCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys

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qq	601 GGCTCCCGCTGGGGAGAGATTCTGAGGATTGTCAGAGCCTGACGCGCACTGTCTGT		
Qy	221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240	À í	581 AlaAspGInCysV
qa	661 GCCGGTGGCTGTGCCCGCTGCAAGGGGCCCACTGCCTGCTGCCATGAGCAGTGT 720	3 <i>8</i>	
ογ	241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	÷ €	801 FIOSEFGIYVAII
ପ୍ର	721 GCTGCCGGCTGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTGCCT	3 8	. Jel 64, 15
ΟŊ	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280	\$ E	
qa	781 AGTGGCATCTGTGAGCTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAG 840	3 8	
Qy	281 SerWetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	À €	277775 T
q		3 8	653
Oy	301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320	3 8	
qa	901 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCTCGTCTGCCCCCTGCACAACCAA 960	20 3	
0y	321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340	ò 2	0033 - 1000 0033 - 1000
qa	961 GAGGTGACGAGGAGGATGGAACACAGGGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1020	3 8	
Qy	341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360	7 A	2101 ACACCTAGCGGAC
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Qy	361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380	7 F	100 K
qa	1081 ATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGC 1140	20 .	ZIOI AGGAAGGIGAAGG
ò	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	δλ	653
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58:	1. AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 	1800
601	1 ProSerGlyValLySProAspLeuSerTyrMetProIleTrpLySPheProAspGluGlu	620 1860
186	1. GlyalaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 	640
64	1 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	53
192	1 GCTGCCCCGCCGAGAGAGCCAGCCTCTGACGTCC	1980
65.	3	653
198	1 ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
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204	1 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	2100
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2101	1 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG	2160
65:	3	653
216	1 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTTGGCACAGTCTACA	2220
65:	3	653
222	1 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC	2280
65:	3	653
228	1 CCCAAAGCCAACAAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2340
65.	33	653
234	1 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACAC	2400
65.	3	653
2401	1 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG	2460
92:	3	653
246	1 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG	2520
65	3	653
252	1 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCCAACCATGTCAAA	2580
65.	3	653
258.	1 ATTACAGACTTCGGGCTGGCTGCTGCTGGACATTGACGAGACAGAC	2640
65:	3	653
264	1 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGGGGTTCACC	2700
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270	1 CACCAGAGTGATGTGGGGGTTATGGTGTGTGTGTGGGGGGCTGATGACTTTTTGGGGCC	2760
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276:	1 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG	2820

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                                                                                                                     GAGGAGTATCTGGTACCCCAGCAGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG
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                                                                                                                                                                                                                                                                                                          ArgProalaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal
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                                        2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC
                                                      -GlnAsnGluAspLeuGlyProAlaSerProLeu
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1. 3768

// Organism="Homo sapiens"
// Xmol_type="genomic DNA"
// Axef="taxon:9606"

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// Thote="unmand protein product"
// Codon_start=1
// Per genomic DNA"
// Protein_id="CAD42363.1"
// Protein_id="CAD42364"
// Protein_id="CAD4264"
// Protein
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Patent: WO 0213847-A 1 21-FEB-2002;
CORIXA CORPORATION (US)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120 	121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140 	141 GInLeuargSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160 	161 LeucysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180 	181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200 	201 GlyserargCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220 	221 AladlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240 	241 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260 	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280 	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300 	301 TyrasnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 	321 GluValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340 	341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn.360 	361 IleGlnGluPheAlaGlyCysLysLysLlePheGlySerLeuAlaPheLeuProGluSer 380 	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400 	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420 	421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440 	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460 	.ySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 48
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1381	CIGGGCAGIGGACIGGCCCTCAICCACCAAAACCCCACCTCTGCTTCGTGCACGGTG 1440	
481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	
501 1501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520 	
521 1561	Glyglnglucys 54 	
541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560 	
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601 1801	ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620 	
621 1861	GlyAlacysGlnProcysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640 	
641 1921	641 GlycysProAlaGluGlnArgAlaSerProLeuThrSer	
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1981	ATTCTGCTGGTCGTGTTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040	
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2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	
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653	653	
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653	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

oy ob	653	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
ob Oy	2521	
QY		
	653	653
Оb	2581	ATTACAGACTTCGGGCTGGCTGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
ΟŊ	653	
qq	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGGCGGCGGTTCACC 2700
ΟŊ	653	653
qa	2701	CACCAGAGTGATGTGGGGAGTTATGGTGTGACTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy	653	653
qa	2761	AAACCTTACGATGGGATCCCGGGGAGGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG 2820
δy	653	653
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d D	3061	
λo ·	705	GlyMetValHisHisArgHisArgSerSerSerSerThrArgSerGlyGlyGlyAspLeuThr
q _O	3121	
δλ	725	LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
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ογ	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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δ	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
QΩ	3421	
Qγ	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLySAsnGlyVal 844
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οy	845	VallysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
QQ	3541	

31-AUG-2000 Unknown.

Unknown.

Unclassified.

Unclassified.

VE 1 (bases 1 to 4473)

ORS Bennett, C.Frank., Lipton, A. and Witters, L.M.

ORS Bennett, C.Frank., Lipton, A. and Witters, L.M.

Antisense oligonucleotide modulation of human HER-2 expression

RNAL Patent: US 5968748-A 1 19-007-1999,

Location/Qualifiers

1. 4473

1. 4473

1.ism="unknown" 859 t 414 101 ileValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120 534 234 294 354 20 40 9 80 PAT linear 4473 919 0 0 336 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: DNA AR080259 4473 bp Sequence 1 from patent US 5968748. AR080259 AR080259.1 GI:10006994 6.37e-187 4900.00 73.23% 73.23% 96.49% 19) x AR080259 (1-4473) imilarity: 1 Similarity: Scores:

GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160

CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG LeuCysTyrGlnAspThr1leLeuTrpLysAsp1lePheHisLysAsnAsnG1nLeuAla
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6	TCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 27.
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2755	ATTACAGACTTCGGGCTGGCTGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2814

17-DEC-2001

PAT

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GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln
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                                linear
CCTACGCCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Kipps, T.J. and Wu.Y.
Vaccines with enhanced intracellular patent: US 6287569-A 26 11-SEP-2001;
Location/Qualifiers
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                                4473 bp
US 6287569
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                                                                                                                          /organism="unknown"
1383 c 1329 g
                                        patent
                               AR167390
Sequence 26 from patent
AR167390
AR167390.1 GI:17903168
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                                                                                                                   3055 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC
                                                                                                                                                                                   GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
                                                                                                                                                                                                                                       LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly
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Db 1855 TIGCCGIGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 1914	Oy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620	Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640 111111111111111111111111111111111111	Oy 641 GlycysProAlaGluGlnArgAlaSerProLeuThrSer	Qy 653 653 Db 2155 ATTCTGCTGGTCGTGGTGTTTGGGGTGTTTTGGGATCCTCATCAAGCGACGGCAGCAG 2214	Qy 653	Oy 653 653 DD 2275 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGACGACGTG 2334	y 653 653 b 2335 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2394	y 653 653 b 2395 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAACACATCC 2454	Y 653 653 b 2455 CCCAAAGCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2514	653	Y 653 653 b 2575 ATGCCCTATGGCTGCCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2634	y 653 653 b 2635 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694	y 653 653 b 2695 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2754	y 653 653 b 2755 ATTACAGACTTCGGGTGGTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2814	y 653 653 b 2815 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2874	y 653 653 b 2875 CACCAGAGTGATGTGGAGTTATGGTGACTGTGTGGGGAGCTGATGACTTTTGGGGCC 2934	ү без 653 653 653
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201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220 	1 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	41 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	61 SerGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 	81 SerMetProAsnProGluGlyArgTyThrPheGlyAlaSerCysValThrAlaCysPro	301 TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 	1 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	1 ValcysTyrclyLeuglyMetGluHisLeuArgCluValArgAlaValThrSer 1 ValcysTyrclyLeuglyMetGluHisLeuArgGluValArgAlaValThrSer 1	nGluPheAlaGlyCysLysLysllePheGlySerLeuAlaPheLeuProGluSer	1) AICLANGAGIIIGCIGGCIGGCAAGGAGGAICIIIGGGAGGCCIGGCAAITTCIGGCCG 81 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGln 	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	AspleuSerValPheGlnAsnLeuGlnVallleArgGlyArg1leLeuHisAsnGlyAla 	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460 	alHisThrVal IGCACACGGTG	ProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	1 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	1 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	1 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	53 GIOGNACON INCLOCARO INCLOCARO COLLOCARO CONTROLO CARALLO CAROLLO EL LEUPROCYSHISPROGLUCYSGINPROGLU ASSOCIATION
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٥y	- 629		nos
qa	2995 C	CTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3054	5
ΟY	653 -		REF
Db	3055 A	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTCTCTGAATTCTCCCGCATGGCC 3114	a, i
٥y	654 -		F .
DP	3115 A	AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	2 2
Qy	665 A	AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	REF
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Οy	685 G	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704	.O.≥
QQ	3235 G	AGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGG 3294	. ב
٥y	705 G	GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724	
QQ	3295 G	SCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGACCTGACA 3354	41.4
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οy	785 P	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804	
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οy	865		
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Д	3835 T		
Qy	905 P	roThralaGluAsnProGluTyrLeuGlyLeuAspValProVal 919	
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RESULT 8			

PRI 30-MAR-1995

linear

mRNA

4473 bp

Human c-erb-B-2 mRNA. X03363

DEFINITION ACCESSION VERSION KEYWORDS

HSERB2R

HSERB2R

203163.1 GI:31197 cell surface glycoprotein; cellular oncogene; erB-2 cellular;

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LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRT
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SWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The c-erb-B-2 protein shows similarity to the epidermal growth
factor receptor.
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Yamamoto, T., Ika473)

Yamamoto, T., Ika473, Akiyama, T., Semba, K., Nomura, N.,

Miyajima, N., Saito, T. and Toyoshima, K.

Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor

Nature 319 (6050), 230-234 (1986)
glycoprotein; growth factor receptor; kinase; neu cellular oncogene; transmembrane protein; tyrosine kinase.
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G to A polymorphism at amino acid codon 655 of the human
erbB-2/HER2 gene
Nucleic Acids Res. 19 (19), 5452 (1991)
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'product-"put. c-erb-B-2 protein (aa 1-1234)"
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CCCAGGGGTGTGAAACCTGTACCTGTACATGCCCATCTGGAAGTTTCCAGATGAGGGGGGGG	6 6 6 6	3 4 3 4 6	o da 6	à a ò a	40 A0	40 60 60 60 60 60 60 60 60 60 60 60 60 60	Qy Db AX0607 LOCUS DEFIN	KEYWOI SOURCE ORGA REFERE AUTE TITI
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Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744	3241 GCTGGCTCCGATGTATTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCCAAAGC 3 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 7 111111111111111111111111111111111111	785 ProserGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnBroGluTyrVal 8 	Qy 805 ASGINProAspValArgProGINProProSerProArgGluGlyProLeuProAlaala 824	Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyiysAsnGlyVal 844	845 ValLysaspValPhealaPheGlyGlyAlaValGluAsnProGluTyrieuThrProGln 86 	Oy 865 GlyGlyAlaAlaProGlnPrOHisProProProAlaPheSerProAlaPheAspAsnLeu 884	Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPhelysGlyThr 904	Qy 905 ProthrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919	RESULT 10 AX467229 LOCUS AX467229 LOCUS AX467229 DEFINITION Sequence 3 from Patent W00234287. ACCESSION AX467229		EFERENCE 1 AUTHORS Beier, A.M., Gautam, A. and Mouritsen, S.R. TITLE Novel therapeutic vaccine formulations JOURNAL Patent: WO 0.034287-A 3 02-MAY-2002; Pharmexa A/S (DK)	FEATURES Location/Qualifiers 1. :30urce 1. :Arganism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
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1561 TGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGTTCCTTCGGGGCCAGGAGTGC 1620	621 GlyAlacysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 6 [611 GlyAlacysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 6 [11	2041 2041 653 2101 653	653	653	2451 GACCTGCTGCTGAACTGCTGTATGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520 653
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VERSION A	4481438.1 GI:22316352	Qy	221
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	ידת מבי	qa	721
TITLE M	reduzer, n., inimier, s., nost, s. and nauwiger, r. ethod for inhibiting the expression of a target gene tent. WO 0705569-a 5-3 18-TITE-2002.	Qy	261
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Qy 101	IleValArqGlvThrGlnLeuPheGluAspAsnTvrAlaLeuAlaValLeuAspAsnGlv 120	δy	461
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0y 121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArqGluLeu 140	Qy	481
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		qa	1561
Qy 181	LeuThrLeuIleAspThrAsnArgSerArgAlaCvsHisProCvsSerProMetCvsLvs 200	٥y	541
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GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln GlySerArgCySTrpGlyGluSerSerGluAspCySGlnSerLeuThrArgThrValCys ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys

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	ate	LL.	ě		Leule	Lysle	AAGC	61yC) 66CT(SerP} TCCTI	ArgG] [[[]] AGGCZ	Tyra] Targ	Alase GCCTC	31 yva 	IleP	ATCT	Cyshi rGCC	CysG]	rgrc?	ProTI	CysLe
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3	Chases 1 to 4530) [pern,M.S. and England llular immunogens comptent: US 6365151-A 4 0 Location/Qualifi 14530	organism="unkno 1382 c 134	1.34e-186 4892.00 73.15% 73.15% 96.34%	7 (1-4530)	AlaAlaLeuCys 	GlnValCysThr	CAAGTGTGCACC	AspMetLeuArg 	TyrLeuProThr 	ValLeuIleAla 	GlythrGlnLeu 	ASNASNTHTTH 	SerLeuThrGlu 	GlnAspThrIle	CAGGACACGATT	IlleaspThrasn 	CysTrpGlyGlu	TGCTGGGGAGAG	CysAlaArgCys 	'CysThrGlyProLy
Unknown. Unknown.	(Cellular in Patent: US	922 a	es: rity: ilarity:	AR20259	MetGluLer ATGGAGCTC	AlaSerTh	GCGAGCACC	ThrHisLer 	GluLeuThi GAACTCACC	GlnGlyTyr CAGGGCTAC	Ilevalare	AspProLet 	GlnLeuArg CAGCTTCG	LeuCysTyr	CTCTGCTAC	LeuThrLeu 	GlySerArg	GGCTCCCGC	Alaglygly GCCGGTGGC	AlaAlaGlyCy
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EYWORDS SOURCE ORGANISM	EFERENCE AUTHORS TITLE JOURNAL EATURES	BASE COUNT ORIGIN	Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity Query Match: DB:	SEQ6 (1-919	Oy Db 1	٥y	Db 2	Oy Db 2	Qy Db 3	Oy Db 3	Qy 1 Db 4	Qy 1 Db 5	Qy 1 Db 5	0y 1	9 qa	Oy 1 Db 6		Dp 40	Oy 2 Ob 8	γ
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                                                                                                                                                                                                                                                                                                                                ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu
                                                                                                                                                                                                                                                                                                             AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
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OV 654	3091 AGGACCCCCAGCGTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCATTGTT 31	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspAetGlyAspLeuValAspAla 6	3151 GALAGCACCTTCTACCGCTCACTGCAGGACGATGACATGGGGGACCTGGTGGATGCT 3	685 GluGluTyrLeuValProGlnGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 7	3211 GAGGAGTATCTGGTACCCCAGCAGGCTTCTTGTGTCCAGACCCTGCCCCGGGCGCTGGG 3	705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyApLeuThr 7	3271 GGCATGGTCCACCACGCCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGACCTGACA 3	725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 7	3331 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGG	Oy 745 AladlySerAspValPheAspGlyAspLeuGlyMetGlyAlaalaLysGlyLeuGlnSer 764	C	VY /0.5 Leurointhisaspiroserrioledinargiyissrildaspirointyalrioled /84	804	3511 CCCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT	100 100 000 0000 0000 0000 0000 0000 0	ous Ashistheroaspvatargkros.hkrobrosekrroargstros.gruptoaata 8	35/1 AACCAGCCAGATGTTCGGCCCCCTTCGCCCCGAGGGCCCTCTGCCTGC	825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 8	3631 CGACCTGGTGCTCTGGAAAGGGCCAAGACTCTCTCCCCAGGGAAGAATGGGGTC 3	845 ValLysAspvalPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 86	_	865 GlyGlyAlaAlaProGlnProHisProProPlaPheSerProAlaPheAspAsnLeu 884		885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904	3811 T	905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspvalProval 919	3871 CCTACGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGT	T 13 481	LOCUS AR283481 4530 bp DNA linear PAT 10-APR-2003 DEFINITION Sequence 1 from patent US 6528060.			ORGANISM Unknown. Unclassified.	REFERENCE 1 (bases 1 to 4530) AUTHORS Nicolette, C.A.	TITLE Therapeutic compounds JOHNAL Patent: US 6528060-A 1	Locatlon/Qualifi te 14530
1951 CCCAGGGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2010	621 GlyalaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640	φ.	2071 GGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTCCATCGTCTGCGGTGGTTGGC 2130	653 653	2131 ATTCTGCTGGTCGTGTTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2190	653 653	2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2250	653 653	2251 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGAG		2311 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2370		2371 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2430		2431 CCCAAAGCAACAAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2490	653 653	2491 TATGTCTCCGGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2550	653 653	2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGGGGACGCCTGGGCTCCCAG 2610	653 653	2611 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG 2670	653 653	2671 CTCGTACACAGGGACTTGGCCGCTCGGAACGTCCTGGTCAAGAGTCCCAACCATGTCAAA 2730	653 653	2731 ATTACAGACTTCGGGCTGGCTGCTGGTGGACATTGACGAGACAGAGTACCATGCAGAT 2790	653 653	2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2850	653 653	2851 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGAGCTGATGACTTTTGGGGGCC 2910	653 653	2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG 2970	653 653	2971 CTGCCCCAGCCCCCCATCTGCATGATGTCTACATGATCATGGTCAAATGTTGGATG 3030	653 653	3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGGAATTCTCCCGCATGGCC 3090
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BASE COUNT ORIGIN	/organism="unknown" 922 a 1382 c 1346 g 880 t
Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil. Ouery Match:	res: 1.34e-186 Length: 4530 4892.00 Matches: 918 arity: 73.15% Conservative: 0 milarity: 73.15% Mismatches: 1 66.34% Indels: 336 Gaps: 1
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631	
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751	
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٥y	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
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oy B	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
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g q	, m	ATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGCCATTCTGCCGGAGAGC	0
ρy	381	heAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
qq	1291	TTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGAGCAGCTCCAAGTGTTT	1350
λα		GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpPrOAspSerLeuPro	420
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qa	1411	accicagegicitecagaaccigeaagiaaiceggggaegaaticigeacaaiggege	1470
ΣŽ	441	TrpLeuGlyLeuArgSerLeuArgGlu	460
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λά	461	SLeuCysPheValHisThrVal	480
qq	1531	SGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTTTCTT	1590
γα	481	neArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	200
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λζ	501	lyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
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ργ	521	3lnPheLeuArgGlyGlnGluCys	540
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qo	1771	GGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT	1830
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qc	1951	CCAGCGGTGTGAAACCTGACTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2010
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q Q	_	CGCATGCCAGCCTTGCCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGATGACAA	2070
λ	641		53
q Q	2071	CTGCCCGCCGAGCAGAGAGCCAGCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC	2130

	745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 7	765 LeuProThrHisAspProSerProJeuGlnArgTyrSerGluAspProThrValProLeu 784 111111111111111111111111111111111111	3511 CCCTCTGAGACTGATGGCTACGTTGCCCCCTGACCTGCAGCCCCAGCCTGAATATGTG 35 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 82	y 825 ArgronlaGlyAlaThrLeuGluArgProLySThrEuSerFroGlyUySAshGlyVal 844	3691 865 3751	885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904	b 3871 CCTACGCCAGAGAACCCAGAGTACCTGGGTCTGGACGTG 3915 ESULT 14 X.882577 AX282577 4530 bp DNA linear PAT 02-NOV-2001 CCESSION AX28257.1 GI:16609668	Σ	TITLE Therapeutic compounds JOURNAL Patent: WO 0168677-A 1 20-SEP-2001; GANZYME CORPORATION (US) LOCALION/QUALIFIERS 1. 4530 Anganism="Homo sapiens" Anol_type="genomic DNA" Ab_xref="taxon:9606" CDS
GCAG 2190 Db GCAG 2190 Qy GCTG 2250 Db GCTG 2250 Qy GCTG 2250 Db	e.			ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCTGGGCTCCCAG 2610 OY OY OY OY OY OY OY OY OY O	TGCGG 2670 Db 3	o o o o		AAACCTTACGATGGGATCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2970 KEYWORDS SOURCE ORGANISM ORGANISM CTGCCCCAGCCCCCATGATGTTGATGTTACATGATCATGGTCAAATGTTGGATG 3030 REFERENCE AITHORS	ATTGACTCTGAATGTCGGCCAAGGTTGGTGTCTGAATTCTCCCGCATGGCC 3090 FEATURES
	2231 653 2311	Oy 653	Db 2431 CCCAAAGCCAACAACAAAATCTTAGA Qy 653	Oy 653	2611	2671 653 2731		Db 2911 AAACCTTACGATGGATCCCAGCCCC Qy 653	Qy 653 Db 3031 ATTGACTCTGAATGTCGGCCAAGAT Qy 654 3091 AGGGACCCCCAGCGCTTTGTGGTCAT Qy 665 AspSerThrPheTyrArgSerLeuLe Qy 665 AspSerThrPheTyrArgSerLeuLe Db 3151 GACGCACTCTACCGCTCACTGCT Qy 685 GluGluTyrLeuValProGlnGlnGlnGl

Fri

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BASE COUNT ORIGIN

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.34e-186 4892.00 73.15% 73.15% 96.34% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: Pred. No.: Score:

918 0 1 336

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	2	643
AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	දි අ	71 CTGCCCCAGCCCCCCATCTGCATTGATGTCTACATGATCATGGTCAAAATGTTGGATG 30
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Glydlacysclintercorpus Association (1974) 11 (Qy	654
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0.000 0.000	δο ¹	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspFroAlaProGlyAlaGly 704
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653 653	7 E	3.1 CTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
2251 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGGGGGGTG 2310		745 Alecticoccascon Dicascon Independent and I
653 653	Š - ₹	4.0 Atao.17se.tabyaarineasyo17saybedo17seco17se.co17se.tahaatau3so17seco15so1 - - - - - - - - - - - -
2311 AGGAAGGTGAAGGTGCTTGGGTGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2370	3 8	10.1 OCIOCOLICONIONILI ONI OGLOPICO CONTO
653 653	Š 1	00 DEUKTOTII NEBASPYLOOBELYLOOBELYLOOBELIN 919-5-5-6-10-10-8-5-7-0-10-10-10-10-10-10-10-10-10-10-10-10-1
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653 653	δ d	/85 PIOSETGIUITIASPOLYTYVAIALAPTOLEUTIIC/SSELFIOGIUF/TOGIUTYVAI 004
2431 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2490	an ü	1 CCCTCTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
653 653	Å to	805 ASIGARPIOASOVALATGPIOGAINPIOPPOSERFIOATGOLUGAJVFTOLEUFIOALAAATA 0.24 [111111111111111111111111111111111111
2491 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2550	qr -	1 AACCAGCCCAGTCGGCCCCCAGCCCCCGAGAGGGCCCTTCTGCCTGC
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653 653	ζ d	
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653 653	Cy St	
2671 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTCAAGAGTCCCAACCATGTCAAA 2730	ar ·	31 GGAGGAGCTIGCCCCTCAGCCCCTCCTTCCTIGCCTTTCAGCCTTCGAGAACCTC 301
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653 653	δ d	900 FIGINITALMETURSHFIOOLUTYTHEUNSPYMIFIONAL 919
2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGGCGGCGGTTCACC 2850	QQ .	30/1 CCIACGGAGGAGCCCAGGGACCIGGGACGIGIGGGACGIGCAGIG
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of primary breast carcinomas using arrays
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Gene expression profiling of primary
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QY	78	2
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16, 2003, 11:05:33

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nuc	OM protein - nucleic search, using frame_plus_p2n model
Run on:	October 15, 2003, 22:47:19; Search time 461.761 Seconds (without alignments) 3105.423 Million cell updates/sec
Title: Perfect score: Sequence:	SEQ5 326 1 QNEDLGPASPLDSTFYRSLLGFFCPDPAPGAGGMVHRHR 59
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Listing first 45 summaries

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ALIGNMENTS

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Homo sapiens Sukaryota: Metazoa; Chordata; Craniata; Vertebrata: Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 378)

REFERENCE

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EST; expressed sequence tag.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-E-CK1-afk-o-11-0-UI.rl UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afk-o-11-0-UI 5', mRNA sequence.
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                                        Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: Ggong@medicine.umaryland.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242 Tel: 319 335 92565
Yang, R.-Z., Shuldiner, A. and Gong, D.-W. EST analysis of human adipose gene expression
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Mismatches:
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BACKWARD: AATACGACTCACTATAGGGCGAATTGG
Seq primer: GTTGGTACCCGGGAATTC.
Location/Qualifiers
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 AUTHORS
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/Glome="UT-E-CK1-age" Retina Foveal and Macular"
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/lone_lib="UI-E-CK1"
/clone_lib="UI-E-CK1"
/clone_li
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Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iow CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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09-MAY-2003 (Rel. 75, Last updated, Version 1)
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Matches:
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/db_xref="taxon:9606"
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Best Local Similarity:
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Location/Qualifiers

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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                        Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                             21C Frontier Korean EST Project 2001
Unpublished
                                                                                                                                                                            Figure 1 yongsung@mail.kribb.re.kr
Plate: 19 row: D column: 03
High quality sequence stop: 531.
                                                                                                                                                             Fax: +82-42-860-4409
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                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/mal_type="mRNA"
/mal_type="mRNA"
/organisme="homo sapiens"
/clone="bkr2p686M12198"
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/dev_stes Sfila + Sfilb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 bp mRNA linear EST 06-MAR-2002
K-EST0103592 S21SNU520s1 Homo sapiens cDNA clone S21SNU520s1-19-D03
5', mRNA sequence.
BM830170
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                                                                                                                Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                             No s1 sequence available.
This clone (DKFZp686M12198) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de
                                                                                                                                                          'ubmitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
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Conservative:
Mismatches:
Indels:
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Mammalia; Eutheria;
1 (bases 1 to 531)
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                                Homo sapiens (human)
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Best Local Similarity:
Query Match:
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REFERENCE

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cDNA was synthesized from oilgo dr-selected mRNA by priming with dr-tailed vector. The dr-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama Berg method. The obtained cDNA vector was electroporation of competent cells E. coli Topl0F' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2.000 - 3.000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription
                                                                                                                                                                                                                                                                                         /note="Organ: Stomach; Vector: pT218RP1; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli ToplOF' with electroporation method.
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Matches:
Conservative:
Mismatches:
Indels:
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/clone_lib="S21SNU520s1"
                                                                                  /clone="S21SNU520s1-19-D03"
/organism-"Homo sapiens"
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149 c 166 q 1
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/db_xref="taxon:9606"
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                                                                                                                 /sex="F"
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SEQ5 (1-59) x CB129403 (1-536)
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BM787824
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                                                                                                                                                                    CB129403 536 bp mRNA linear EST 29-JAN-2003 K-EST0179037 CLSNU17 Homo sapiens CDNA clone CLSNU17-5-C08 5', mRNA
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 536)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Far: +82-42-866-4470
Fax: +82-42-860-4409
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Mismatches:
Indels:
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Matches:
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/clone="CLSNU17-5-C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: yongsungemail.kribb.re.kr
Plate: 5 row: C column: 08
High quality sequence stop: 536.
Location/Qualifiers
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/lab_host="Topl0F'"
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CB129403.1 GI:28093000
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Best Local Similarity:
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K-EST0103390 S21SNU520s1 Homo sapiens cDNA clone S21SNU520s1-17-C05
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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                                  Conservative:
Mismatches:
Indels:
Gaps:
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Plate: 17 row: C column: 05
High quality sequence stop: 574.
Location/Qualifiers
1. 574
/organism="Homo sapiens"
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/db_xref="raxon:9606"
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Unpublished
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Best Local Similarity:
Query Match:
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The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 356 7171
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Subtracted with brain, liver, lung, kidney and muscle.
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Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.

a 272 c 243 g 155 t
                                                                                 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCap"
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM492 row: j column: 17
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NIH-MGC http://mgc.nci.nih.gov/.
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AGENCOURT_14364504 NIH_MGC_181 Homo sapiens cDNA clone IMAGE:30408904 5', mRNA sequence.
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                                                                                                                        , LNCAF
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CD516283.1 GI:31448001
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Homo sapiens
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                                                                                                                                             /tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/cloom_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
bento-soares@dulowa.edu
TAG_SEQ=None found.
131 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA489799 849 bp mRNA linear EST 14-NOV-2002 AGENCOURT_10810428 MAPCL Homo sapiens CDNA clone IMAGE:6722285 5', CA489799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Robert Strausberg, Ph.D.
Email: Gapba-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
ffound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 539.
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                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Seq primer: M13 FORWARD POLYA=No.
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EST 06-JUN-2003

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 893)

S NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://mage.llnl.gov

Plate: LLAMI488 row: 1 column: 23
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/clone="IMAGE:6722663"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
                                            /clone_lib="Maper" // Action | Action |
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Location/Qualifiers
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/clone_lib="MAPcL"
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CA455141.1 GI:24905561
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Best Local Similarity:
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             /organism="Homo sapiens"
/mol_type="mkNA"
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/clone="IMAGE:30408904"
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(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."
59 a 288 c 247 g 156 t
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AGENCOURT 10735919 MAPCL Homo sapiens CDNA clone IMAGE:6722585 5',
mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 885)

NIH-MGC http://mgc.nci.nih.gov/

National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14285 row: i. column: 17
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Location/Qualifiers
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CA455074.1 GI:24905427
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Best Local Similarity:
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/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dr. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Rungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA454131 894 bp mRNA linear EST 12-NOV-2002 AGENCOURT_10738550 MAPCL Homo sapiens cDNA clone IMAGE:6718792 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM14275 row: k column: 16
High quality sequence stop: 636.
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/clone_lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site_l: ECORV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dr. Average
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NIH-WGC http://mgc.nci.nih.gov/.
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/organism="Homo sapiens"
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/clone="IMAGE:6718792"
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CA454131
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TITLE
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COMMENT
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EST 11-JUN-2003
insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted.

1 303 c 260 g 151 t
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//mol.type="mRNA"
//mol.type="mRNA"
/db_xref="taxon:9606"
/clone="InAGE:30396412"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="PH10B-Ton A ( Tl and T5 phage resistances)"
/clone=lib="NH1LMG_181"
/note="Vector: pCMV-SPORT6.1; Site_1: Not1; Site_2: ECORV (destroyed); Library is oligo-dT primed and directionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 GAGGACGATGACATGGGGGACCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGC 143
                                                                                                                                                                                                                                                                                                                                                21 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 899)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmlOA70 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMA78 row: b column: 05
High quality sequence start: 47
High quality sequence stop: 443.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCOURT_14476827 NIH_MGC_181 Homo sapiens cDNA clone IMACE:30396412 5', mRNA sequence.
CD558386 GI:31584454
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Conservative:
Mismatches:
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Homo sapiens
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CD558386
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CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

http://image.lni.gov

Plate: LLCM2781 row: j column: 04

High quality sequence stop: 654.

Coation(Vaulifiers

1. 916

/ Organism="Homo sapiens"

/ Mol_Ltype="mRNRN"

/ Ab_xref="taxon:966"

/ Clone="IxAGE:6578980"

/ Lissue type="teratocarcinoma, cell line"

/ lab_host="NHLMGE:109"

/ clone_lib="NHLMGE:109"

/ clone_lib="NHLMGE:109"

/ note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:

Xhoi: coll Lib="NHLMGE:109"

/ clone_lib="NHLMGE:109"

/ clo
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1 (bases 1 to 916)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU845369
AGENCOURT_10416348 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:578980 5′, mRNA sequence.
                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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BU845369.1 GI:24029810
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326.00
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Best Local Similarity:
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                                                                                                                                                        Scores:
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                                                                          BASE COUNT
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BU845369
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TITLE
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Search completed: October 16, 2003, 17:04:51 Job time : 463.761 secs

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Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 124, Appli
Sequence 125, Appli
Sequence 125, Appli
Sequence 125, Appli
Sequence 126, Appli
Sequence 17, Appli
Sequence 11, Appli
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Sequence 1, Appli
Sequence 1731, Ap
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PLCJ
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
2 US-10-378-393-14

0 US-09-930-125-6

0 US-09-930-125-7

0 US-09-930-125-7

0 US-09-930-125-7

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2 US-10-378-39-10

2 US-10-378-39-10

US-09-811-115-2

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0 US-09-811-115-1

1 US-09-811-115-1

2 US-10-101-510-81

4 US-10-101-510-81

2 US-10-101-510-81

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2 US-10-101-510-124

2 US-09-769-508-1

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2 US-09-111-12-1
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0 US-09-874-356-10

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0 US-09-860-352-4186

US-09-725-433-1

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2 US-10-039-926-1731

3 US-10-039-926-1731

2 US-10-101-510-98

0 US-09-974-298-98

0 US-09-974-298-98
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Publication No. US20030054421A1
GENERAL INFORMATION:
   50055330
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33768
33768
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4606
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SOFTWARE: Patentin Ver.
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (390)
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US-10-102-806-165
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LENGTH: 111
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   Sequence 165, App
                                                                                                     October 16, 2003, 11:08:07; search time 60.9885 Seconds (without alignments) 2540.503 Million cell updates/sec
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1 QNEDLGPASPLDSTFYRSLL......GFFCPDPAPGAGGMVHHRHR 59
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2. /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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17. /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

    nucleic search, using frame_plus_p2n model

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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Coever, Martin A.
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Alos, Michael J.
APPLICANT: Malos, Michael D.
APPLICANT: Morbill, Patricia D.
APPLICANT: Morbill, Patricia D.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
TITLE OF INVENTION: COP HER 2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Codes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: McNeill, Partraia
APPLICANT: McNeill, Partraia
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: OF MPE-Z/NEU-ASSCIATED MALIGNANCIES
TITLE OF INVENTION: OF MPE-Z/NEU-ASSCIATED MALIGNANCIES
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT APPLICATION NUMBER: US/09/930,125
SOFTWARE: FREIL SEQUENCE: 2012-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FREILSED FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1033 TTCTTCTGTCCAGACCCTGCCCGGGCGCTGGGGGCATGGTCCACCACAGGCACGCC 1089
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Matches:
Conservative:
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                                                          US-09-930-125-6
; Sequence 6, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09930125; Publication No. US20020193329A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326.00
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CRGANISM: Homo sapiens
US-09-930-125-4
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Best Local Similarity:
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LENGTH: 1767
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Sequence 14, Application No. US20030182668A1

GENERAL INFORMATION:

APPLICANT: BOJ, David K.

APPLICANT: BOJ, David K.

APPLICANT: BOJ, Tai W.

APPLICANT: Hong, Tai W.

APPLICANT: Hong, Tai W.

APPLICANT: Hong, Tai W.

TITLE OF INVENTION: TYROSINE KINASE RECEPTORS

CURRENT APPLICATION NUMBER: US/10/378, 393

CURRENT APPLICATION NUMBER: US 60/360, 889

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 23

SOGTWARE: PatentIn Version 3.2

SEQ ID NO 14
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; OTHER INFORMATION: n equals a,t,g,;
NAME/KEY: misc_feature
LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g,
US-10-102-806-165
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; ORGANISM: Homo sapiens
US-10-378-393-14
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Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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LENGTH: 1713
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Sequence 7, Application US/09930125
Sequence 7, Application US/09930125
Sequence 7, Application No. US20020193329A1
SEDIGATION US US20020193329A1
SETURAL INFORMATION:
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Lodes, Michael J.
APPLICANT: Kalos, Michael D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Wordil, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.344
CURRENT APPLICATION NUMBER: US/09/930,125
UNDER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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59
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         1767
59
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         Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Homo sapiens
US-09-930-125-7
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Best Local Similarity:
Query Match:
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Alignment Scores:
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US-09-930-125-5
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RESULT 7
US-10-378-393-10
Sequence 10, Application US/10378393
Publication No. US20030182668a1
GENERAL INFORMATION:
APPLICANT: Carboni, Joan M.
APPLICANT: Rowley, Ronald B.
APPLICANT: Wong, Tai W.
APPLICANT: Hee, Francis Y.
TITLE OF INVENTION: TRANSGENE KINASE RECEPTORS
FILE REFERENCE: D0254 NP
CURRENT FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2002-03-01
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APPLICANT: Cheever, Mattin A.
APPLICANT: Lodes, Michael J.
APPLICANT: Ralos, Michael J.
APPLICANT: Ralos, Michael D.
APPLICANT: Wowell, Patricia D.
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                                                                       APPLICANT: Hand-Zimmerman, Susan
Publication No. US20020193329A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
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LENGTH: 2411
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SEQ5 (1-59) x US-09-811-115-2 (1-3768)
        APPLICANT: Ralph Schwall
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| Sequence 5, Application US/10207498
| Publication No. US20030143568A1
| Publication No. US20030143568A1
| GENERAL INFORMATION: MISONATION: M
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; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
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US-10-207-498-5
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Best Local Similarity:
Query Match:
  Best Local Similarity:
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Sequence 2, Application US/09811115
GENERAL INFORMATION:
APPLICANT: Erickson, Sharon
APPLICANT: Erickson, Sharon
APPLICANT: Ring, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENERY: 034A
CURRENT FILICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SCO ID NOSS: 4
SOFFWARE: FastSEQ for Windows Version 4.0
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ETBB
FITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENENT.073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR PALLOATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-06-23
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Mismatches:
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Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 3768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ5 (1-59) x US-09-811-123-8 (1-3768)
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US-09-811-123-8
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                                                                                                                                                                                                                                                                   TYPE: DNA
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DB:
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LENGTH: 3768
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                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3768)
OTHER INFORMATION: human HER-2/neu protein
NAME/KEY: misc_feature
LOCATION: (1)..(1959)
OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2026)..(3765)
OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2968)..(3765)
OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2968)..(3144)
OTHER INFORMATION: preferred portion of the phosphorylation domain
OTHER INFORMATION: (delta PD) of human HER-2/neu
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Mismatches:
Indels:
Gaps:
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APPLICANT: Gheysen, Dirk
APPLICANT: Smithkline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 0.14058-0.09910PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT APPLICATION NUMBER: US 09/493,480
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.1
SEC ID NOS: 26
SEC ID NOS: 26
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Matches:
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Patent No. US20020177567A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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Sequence 1, Application US/08930125

Publication No. US20020193329A1

GENERAL INFORMATION:

APPLICANT: Hand-Zimmerman, Susan

APPLICANT: Cheever, Martin A.

APPLICANT: Lodes, Michael J.

APPLICANT: Monelll, Patricia D.

APPLICANT: Movelll, Patricia D.

APPLICANT: World, Armomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHOOS FOR THE THERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES

TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES

CURRENT PILING DATE: 2001-08-14

CURRENT FILING DATE: 2001-08-14

CURRENT FILING DATE: 2001-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3088 TICTICTGICCAGACCTGCCCGGGGGCGCATGGICALILILILILILILILILILI
3088 TTCTTCTGTCCAGACCTGCCCGGGGCGTGGGGGCATGGTCCACCACAGGCACCGC 3144
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Publication No. US20030157119A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
APPLICANT: Hand-Zimmerman, Susan

TITLE OF INVENTION: MATHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL

TITLE OF INVENTION: AND VIRGS-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.483C3

CURRENT APPLICATION NUMBER: US/10/313,644

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FRSELEQ for Windows Version 3.0
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Matches:
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US-09-930-125-1
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ORGANISM: Homo sapien
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Sequence 5, Application US/09441411

Publication No. US20030008342A1

Sequence 5, Application US/09441411

September 1 Scholler, Nathalie B.

APPLICANT: Scholler, Nathalie B.

APPLICANT: Hellstrom, Ingegerd

APPLICANT: Hellstrom, Karl Erik

TITLE OF INVENTION: SUFFACE RECEPTOR ANTIGEN VACCINES

FILE REFERENCE: 730033.409

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 26

SOFTWARE FALSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 4473
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Matches:
Conservative:
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Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                         SEQ5 (1-59) x US-10-313-644-1 (1-3768)
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ORGANISM: Homo sapiens
             ; LOCATION: (1)...(3765)
US-10-313-644-1
                                                                                  Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                        Percent Similarity:
NAME/KEY: CDS
                                            Alignment Scores:
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| GENERAL INFORMATION:
| APPLICANT: WANG, YIXIN
| TITLE OF INVERTION:
| FILTE OF INVERTION:
| FILTE OF INVERTION:
| CURRENT APPLICATION NUMBER: 05/20, 947
| FRIOR PILING DATE: 200-03-20
| PRIOR PILING DATE: 200-03-20
| SOFTWAREN PALCATION NUMBER: 60/276,947
| FRIOR PILING DATE: 200-03-20
| SOFTWAREN PALCATION NUMBER: 60/276,947
| SECOTE | SOFTWAREN PALCATION NUMBER: 60/276,947
| SECOTE | SOFTWAREN PALCATION NUMBER: 60/276,947
| TITLE OF THE AFT STATEMENT PALCATION NUMBER: 60/276,947
| SECOTE | SOFTWAREN PALCATION NUMBER: 60/276,947
| SECOTE | SOTT STATEMENT PALCATION NUMBER: 60/276,947
| SECOTE |
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Sequence 12244,
Sequence 12104,
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Sequence 3, App
Sequence 6, App
Sequence 51, App
Sequence 191, App
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Sequence 10705,
Sequence 15955,
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Sequence 1
Sequence 1
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Sequence 2
Sequence 4
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US-09-218-4678-1
US-09-218-4678-1
US-09-213-864-1
US-09-792-594-10
US-09-252-991A-12244
US-09-252-991A-12104
US-09-252-991A-12104
US-09-252-991A-16553
US-09-252-991A-16553
US-09-252-991A-16553
US-09-252-991A-16553
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.30
US-09-676-610B-17

US-09-877-177A-10

US-09-364-691-11

US-09-364-691-11

US-08-783-75-3

US-08-783-75-3

US-08-783-77-11

US-08-843-951-11

US-08-843-951-11

US-08-237-401A-3

US-08-237-401A-3

US-08-237-401A-3

US-08-484-438-1

US-09-218-467B-6

US-09-218-467B-6

US-09-170-496D-191

US-09-170-478-601-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sharkey, Richard G.
REGISTRATION UNBER: 32,620
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELERAN: (206) 622-4900
TELERAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY.

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"WITTER: IBM PC compatible
"WITTER: IBM PC compatible
"WITTER: "WARM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
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; Sequence 1, Application US/08625101
; Patent No. 5869445
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3321
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CITY: So
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MODEL-frame+_p20.model - DEV=xlp
-0-/cgn2_J/3DPTO_spool_p/HOLLERAN480/runat_15102003_131913_20570/app_query.fasta_1.4685
-09-/cgn2_J/3DPTO_spool_p/HOLLERAN480/runat_15102003_131913_20570/app_query.fasta_1.4685
-09-/cgn2_J/3DPTO_spool_p/HOLLERAN480/runat_15102003_131913_20570/app_query.fasta_1.4685
-009-STAT-0 - UNITS-bits - START-1 - END-1 - MATRIX-blosum62 - TRANS-human40.cdi
-LIST-45 -DOCALIGN=200 - TRR_SCORE=pct - THR_MAX-IO0 - THR_MIN=0 - ALIGN=15
-MODE-LOCAL - OUTPMT-pto - NORM-ext - HEAPSIZE-500 - MINLEN=0 - MAXLEN=200000000
-USER-HOLLERAN480_cCSN_1_1_403_erunat_15102003_131913_20570 - NCPU=6 - ICPU-3
-NO_MMAP - LARGEQUERY - NGE_SCORES=0 - MINTT - DSPBLOCK=100 - LONGLOG
-DEV_TIMEOUT-120 - WARN_TIMEOUT-30 - THRRADS-1 - XGAPOP-10 - XGAPEXT-0.5 - FGAPOP=6
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1741.185 Million cell updates/sec
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                                                                                                                                 October 15, 2003, 22:55:19; Search time 14.9563 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
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                                                                                                                                                                                                                                                    ......GFFCPDPAPGAGGMVHHRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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US-08-356-786-1
US-09-048-804-1
US-09-056-105-26
US-08-629-515A-9
US-08-645-865-9
US-09-157-322-4
US-09-527-487-1
US-09-877-177A-11
US-08-229-515A-14
US-08-645-865-14
US-08-645-865-14
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                                                                                                                                                                                                                                                                                                                                                                                                     569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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326
1 QNEDLGPASPLDSTFYRSLL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
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44530
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Perfect score:
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Maximum DB
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3088 TTCTTCTGTCCAGACCTGCCCGGGGGCGTGGGGCATGGTCCACACAGGCACCGC 3144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Road, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                   3768
59
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILLING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        SEQ5 (1-59) x US-08-625-101-1 (1-3768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08356786 Patent No. 5877305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                     326.00
100.00%
100.00%
100.00%
                                                                                                                                                                                     3.24e-32
              : 3768 base pairs
nucleic acid
EDNESS: single
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SEQUENCE CHARACTERISTICS
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STATE: Massachusetts
                               TYPE: nucleic ació
STRANDEDNESS: sing
TOPOLOGY: linear
'FEATURE:
                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                ; NAME/KEY:
; LOCATION:
US-08-625-101-1
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3028 GAGGACGATGACATGGGGGACCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGC 3087
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ADDRESSE: Woodcock Washburn Kurtz Macklewicz & No. 5968748ris LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GluaspaspaspMetGlyAspLeuValaspAlaGluGluTyrLeuValProGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09048804
Patent No. 5968748
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION | OF
TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
                                                                                                                                                                                               3768
59
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                                                                                                     ; LOCATION: 1..3768
; OTHER INFORMATION: /note= "product = "cerB-b2""
US-08-356-786-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,804
FILING DATE: Herewith
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Paul K. Legaard
REGISTATION NUMBER: 38,534
REPERENCE/DOCKET NUMBER: ISIS-2913
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          SEQ5 (1-59) x US-08-356-786-1 (1-3768)
                                                                                                                                                                                               3.24e-32
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TYPE: Nucleic Acid
STRANDEDMESS: Single
TOPOLOGY: Unknown
ANTI SENSE: NO
US-09-048-804-1
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                    MOLECULE TYPE: CDNA FEATURE:
                                     linear
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Best Local Similarity:
Query Match:
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                                                                                           NAME/KEY: CDS
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                                                                                                                                                                          21 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40
                                                                                                                                                                                                                         Sequence 26, Application US/09056105
Fatent No. 6287569
GENERAL INFORMATION:
APPLICANT: WILL STRIPS, THOMAS J.
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT FILING DATE: 1998-04-06
EARLIER FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
SEQ ID NO 26
SEQ ID NO 26
TENDER 1473
TOTAL 1473
TOTAL 1473
TOTAL 1473
          Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                 SEQ5 (1-59) x US-09-048-804-1 (1-4473)
          3.96e-32
326.00
100.00%
100.00%
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US-09-056-105-26
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Best Local Similarity:
Query Match:
                                Percent Similarity:
Best Local Similarity:
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Alignment Scores
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US-08-229-515A-9
                                                            Query Match:
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3118 CAGAATGAGGCTTTGGGCCCAGTCCCTTGGACAGCATCTACACCGTCACTGCTG 3177
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; Patent No. 5654406
; GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FALLUL H
TITLE OF INVENTION: REBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
 ERBB2 PROMOTER BINDING PROTEIN IN NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4530
59
0
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                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                   E: NEEDLE & ROSENBERG PC
127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERNCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-0770
TELEPHONE: 404-688-9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ5 (1-59) x US-08-229-515A-9 (1-4530)
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326.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4530 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single;
TOPOLOGY: linear
US-08-229-515A-9
TITLE OF INVENTION: ERE TITLE OF INVENTION: NEC NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                            Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Georgia
COUNTRY: usa
ZIP: 30303
                                                                                        STREET: 127 Pe
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: Georgia
                                                                                                                                           COUNTRY: usa
                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-08-645-865-9
                                                                                                                            STATE:
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21 GluAspAspAetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40
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STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4530
59
0
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLEASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 1414.608
TELEPHONE: 404.688-0770
TELEPHONE: 404.688-0770
TELEPHONE: 404.688-0770
TELEPHONE: 404.688-0770
TELEPHONE: A04.688-080
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: MODOLOGY
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-US-10/1024-4
Sequence 4, Application US/09167322
Setent No. 6365151
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
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Gaps:
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APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-0ct-1998
CLASSIFICATION: cunknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ5 (1-59) x US-08-645-865-9 (1-4530)
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326.00
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ZIP: 19102
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Best Local Similarity:
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21 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40
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Conservative:
Mismatches:
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Mismatches:
        TELING DATE: <ur>
    CURNEY/AGENT INFORMATION:

    NAME:
    NOMER:

    NAME:
    NOMER:

    NOWER:
    NOWER:

    TELECOMMUNICATION
    TELEPHONE:

    TELEPHONE:
    (215)

    SEQUENCE CHARCTERISTICS:

    SEQUENCE CHARCTERISTICS:

    LENGTH:
    4530

    DASE PAIR

    TYPE:
    NUCleic acid

    STYPE:
    NUCLEIC acid

    STRANDEDNES:
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; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
APPLICANT: Nicolette, Charles
TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
LENGTH: 4530
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APPLICATION NUMBER: PCT/US97/00582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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326.00
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Query Match:
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Best Local Similarity:
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LOCATION: (15)
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                                                       CLASSIFICATION:
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STATE: Georgia
                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                      US-08-229-515A-14
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                        3118 CAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTG 3177
                                                                                Sequence 11, Application US/09877177A

Patent No. 6582919

GENERAL INFORMATION:

APPLICANT: K. Danenberg

TITLE OF INVENTION: Method of determining Epidermal Growth

TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression

TITLE OF INVENTION: And Correlation of Levels Thereof With Survival

FILE REFERENCE: 11220/120

CURRENT APPLICATION NUMBER: US/09/877,177A

CURRENT FILING DATE: 2001-06-11

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                       4530
59
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 5518885
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ANDRITTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                   4.01e-32
326.00
100.008
100.008
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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COUNTRY: usa
                                                                                                                                                    US-09-877-177A-11
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US-08-229-515A-14
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2999 CAGAACGAGGACTTGGGCCCATCCAGCCCCATGGACAGTACCTTCTACCGTTCACTGCTG 3058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SARKAR, FAZUUL H
APPLICANT: SARKAR, FAZUUL H
TITLE OF INVENTION: BRBB1 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865 FILING DATE: 14 MAY 1996 CLASSIFICATION: 435
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID 6
REGISTATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 404-688-980
TELEPASK: 404-688-980
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NAME: PERRYBAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ5 (1-59) x US-08-229-515A-14 (1-3955)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
                                                                                                                                                                                                                                     TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279.00
88.14%
84.75%
85.58%
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ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FEATURE:
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Sequence 3, Application US/08475035

Sequence 3, Application US/08475035

Sequence 3, Application US/08475035

Batent No. 2985553

Sequence 3, Application US/08475035

Sequence 3, Application US/08475035

APPLICANT: RRAUS, MATTHIAS H.

APPLICANT: APPLICANT: USA

SCHEEF: Suite 1200, 127 Peachtree Street

COUNTY: Atlanta

STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATE: TSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/475,035
FILING DATE: 7 Jun 1995
CLASSIFICATION: 435
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Conservative:
Mismatches:
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Gaps:
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NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DGOKET NUMBER: 1414.656
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      SEQ5 (1-59) x US-08-645-865-14 (1-3955)
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279.00
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84.75%
85.58%
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            TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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404-688-0770
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                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
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9 SerProLeuAspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeu 28
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Patent No. 6582919

GENERAL INFORMATION:
APPLICANT: K. Danenberg

TITLE OF INVENTION: Method of determining Epidermal Growth
TITLE OF INVENTION: Factor Receptor and HER2 Neu Gene Expression
TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
FILE REFERENCE: 11220/120
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/09676610B
Patent No. 6444465
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REPERENCE: RTS-0138
CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                         29 ValAspAlaGluGluTyrLeuValProGlnGlnGlyPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 ValAspAlaGluGluTyrLeuValProGlnGlnGlyPhePhe
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Indels:
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; LOCATION: (187)...(3819)
US-09-676-610B-17
CDS
187..3816
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-676-610B-17
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                                                                    Alignment Scores:
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              ; LOCATION:
US-08-475-035-3
NAME/KEY:
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Search completed: October 16, 2003, 17:18:38 Job time: 41.9563 secs
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APPLICANT: Fox, Andrew J.
APPLICANT: Fox, Andrew J.
APPLICANT: Jones, Dennis Mackay
TITLE OF INVENTION: Campylobacter
NUMBER OF SEQUENCES: 19
CORRESPONDENCE STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,991
FILING DATE: 29-FEB.1996
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01967
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9318751.6
FILING DATE: 09-SEP-1993
ATORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0040000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION NUMBER: US/09/877,177A
CURRENT FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 197496
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                           SEQ5 (1-59) x US-09-877-177A-10 (1-197496)
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Patent No. 6001565
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                             3.49e-06
138.00
91.18%
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Mismatches:
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88.24%
70.59%
41.72%
                                          Score:
Percent Similarity:
Best Local Similarity:
Query Match:
; MOLECULE TYPE:
US-08-604-991-11
                        Alignment Scores:
Pred. No.:
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2842.104 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Listing first 45 summaries
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Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; Human breast and ovarian cancer associated antigen gene SEQ ID 165. 27-MAR-2001 (first entry) N_Geneseq_19Jun03:*

| SIDS1/gcgdata/geneseqn-embl/NR1980.DAT:*
| SIDS1/gcgdata/geneseqn-embl/NR1981.DAT:*
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Mouse Her-2∕neu cD

ALIGNMENTS

AAF21778 standard; DNA; 1115 BP

AAF21778 RESULT 1

AAA89737

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

AAD32746;

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proteins AAB58711 - AAB59128. The DNA and protein sequences are proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the sequences AAF22040 and AAB59129 which are used in the invention and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; no corropic; neuroprotective; antiblicytal; antitaliergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidiabetic; and protein sequences are used in the diagnosis of particularly breast and ovarian cancer. The nucleic acid sequences, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, continuation of the anaemia, autoimmune thyroiditis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArg
cardiovascular disorder; wound healing; neurological disease; ds.
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                                                                                                                                     08-MAR-2000; 2000WO-US05881.
                                                                                                                                                                     99US-0124270.
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P-PSDB; AAB58875.
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                                                                  WO200055173-A1
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                                    Homo sapiens.
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukcoyte antigen (HLA) B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for human malignancies, for stimulating and/or expanding T cells specific for human patient, as probe or primer for nucleic acid hybridisation, to patient. The invention is useful for stimulating a T cell response in a patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in gene therapy. The preferably for the immunotherapy of breast cancer and other Her-2/Neu-

ssociated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_native_coding_region.
                                                                                                                     Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss
                                                                                                                                                                                                                                                                    /product= "Human protein encoded by cDNA for the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
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                                                                                                                                                                                                                                                                                 HICD_native_coding_region"
/transl_except= (pos:1741..1752, aa:Leu-Glu)
/note= "CDS does not include stop codon"
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                                                                                    Human cDNA for the clone HICD_native_coding_region.
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Mismatches:
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1..1755
/*tag= a
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                                                  (first entry)
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Mcneill PD, Vedvick TS;
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Best Local Similarity:
Query Match:
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Example 5; Page 119; 129pp; English
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11D AAD3

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BDE Huma

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                                                                                                                                                                                                                                                                        1006 GAGGACGATGACGACCTGGTGGAGGTGCTGAGGATTCTGGTACCCCAGCAGGC 1065
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                                                                                                                                                                                                                                    GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40
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/product= "Human protein encoded by cDNA for the clone
HICD_CT_His_coding_region"
                                                                                                GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA for the clone HICD_CT_His_coding_region.
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1..1764
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                        SEQ5 (1-59) x AAD32746 (1-1755)
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Mcneill PD, Vedvick TS;
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P-PSDB; AAE20481.
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cancer,
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human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cance preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_CT_His_coding_region.
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/product= "Human protein encoded by cDNA for the clone
HICD_in_pPDM_coding_sequence"
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                                                                                                                     529 G; 336 T; 0 other;
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59
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Mismatches:
Indels:
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Matches:
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                                                                                                                     Sequence 1767 BP; 381 A; 521 C;
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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Mcneill PD, Vedvick TS;
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P-PSDB; AAE20484.
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Best Local Similarity:
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The composition is useful for the diagnosis, prevention of cancer. The compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating ar cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in the feratment of cancer, preferrably for the immunotherapy of breast cancer and other Her-2/Neu-second and in gene therapy. The former and content the immunotherapy of breast cancer and other Her-2/Neu-second and patient and in gene therapy. The former and content the former for an expression of a second and alignancies. The invention is useful in gene therapy. The former former is human cDNA for the clone HICD_in_ppbM_coding_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1090 TICTICIGECCAGACCTGCCCGGGGGCGCATGGTCCACCACAGGCACGC 1146
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HICD_plus_8_HIS"
/transl_except= (pos:1543..1545, aa:Pro)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1773 BP; 383 A; 528 C; 530 G; 332 T; 0 other;
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Matches:
Conservative:
Mismatches:
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Gaps:
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1..1803
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Best Local Similarity:
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HiA)-144 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for the Taylou polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a length gene from a suitable library, and confined to a sectul in appropriate host cells. The composition is useful in complement to the treatment of confined to the composition of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prophylactic or therepoutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_plus_0_HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
                                                                                                                                                                                                                                                                                                                                           Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
                                                                                                                                                                                   Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1806 BP; 391 A; 530 C; 544 G; 341 T; 0 other;
                                                                                                                                                                                   Cheever MA, Foy TM, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 118; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA89736 standard; DNA; 3600 BP.
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326.00
100.00%
100.00%
                   14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-59) x AAD32745 (1-1806)
                                                                                                                                                                                Hand-zimmermann S, Chee
Mcneill PD, Vedvick TS;
                                                                                                                                                                                                                                                               WPI; 2002-280758/32
                                                                                                                                 (CORI-) CORIXA CORP
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cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepadnavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
                                                                                                                                                                                                                                                    /product= "Breast cancer antigen Her2 variant"
                                               cDNA encoding human breast cancer antigen, Her2 variant
                                                                              cytostatic; antiviral; immunostimulant;
                                                                                                                                                                                                       Location/Qualifiers
7..3678
/*tag= a
                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001; 2001WO-US45626,
                   24-SEP-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              (MINC/) MINCHEFF
(LOUK/) LOUKINOV
(ZOUB/) ZOUBAK S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU98923.
                                                                                                                                                                                                                                                                                     WO200240059-A2
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                                                                                 Human; Her2;
                                                                                                                                                                            Homo sapiens.
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3088 TICTICITCTCCAGACCTGCCCGGGGGCGCATGGTCCACCACAGGCACCGC 3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes the human HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and proster cancers, and may be used as an antigen to vaccinate against
                                                                                                                                                                                                                                                                                                                                                                                                          HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArg 59
   prostate cancer; ovarian cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3600 BP; 723 A; 1108 C; 1075 G; 694 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                        /product= "HER-2/neu protein"
                                                                            Location/Qualifiers
1..3600
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 15; 128pp; English.
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326.00
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100.00%
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(SMIK ) SMITHKLINE BEECHAM.
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P-PSDB; AAB21198, AAB21208.
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                 colon cancer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               these neoplasias
breast cancer;
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                                                sapiens.
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                                                Homo
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The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, reacting a subject having undeasted cells, for example tumour cells. Creating a subject having undeasted cells, for example tumour cells or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynoutcleotide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and leukaemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lentiviruses and the flaviviruses and pestiviruses. The present sequence represents the coding sequence of human breast cancer antigen, Her2 variant, used as a target antigen in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                          Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen by a cell, comprises administering a polynucleotide encoding a variant of an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
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Matches:
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Gaps:
                                                                   (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 128-134; 146pp; English.
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                                                                                                                                                                                                                                         Mincheff MS, Loukinov DI, Zoubak
01-NOV-2000; 2000US-0704232.
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326.00
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                                                                                                      MINCHEFF M S.
LOUKINOV D I.
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2878 CAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTG 2937
                                                                                Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbS2) protein (AAM01111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Lys676-Val1255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral vector, for genetic immunisation of an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "nucleotides 2026-3765 (claim 1) code for HER-2/neu intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
                                                                                                                                                                                                                                                                               HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      759 A; 1171 C; 1119 G; 719 T; 0 other;
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59
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Mismatches:
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Matches:
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1..3765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 49-56; 71pp; English
                                                                                                                                                                   AAT40739 standard; cDNA; 3768
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326.00
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                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                     HER-2/neu oncogene.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1995;
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                                                                                                                                                                                              AAT40739
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This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a mailyanancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
                                                                                                                                             Use of HER-2/neu polypeptides - for eliciting an immune response to an HER-2/neu associated malignancy, particularly for treating or
                                                                                                                                                                                                                                                                                                        HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "region which elicits immune response"
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  Indels:
            Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                            /product= "HER-2/neu"
/note= "oncogene"
2026.3765
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..3768
                                                                                                                                                                                                                                                                                                                   malignancy; treatment; tumour; ss.
                                                                                                                                                                                                                 AAX01912 standard; DNA; 3768 BP.
                                                                                                                                                                                                                                                                                 Human HER-2/neu oncogene DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
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100.00%
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                                 (1-59) x AAT40739 (1-3768)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing tumours
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                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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12-AUG-1993;
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  Query Match:
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                      The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-rassociated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and
                                                                                                                                                                                                                                                        Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor associated
                                                                                                                                                                                                                                                                                                                                                                                                                                         Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide antigens for the treatment of breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nielsen KG, Haaning J, Leach D,
Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human heregulin 2 (Her2) coding sequence.
                                                                                                     Gaps:
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Karlsson G;
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P-PSDB; AAY92620.
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                                                              Percent Similarity:
Best Local Similarity:
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                        Alignment Scores:
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3028 GAGGACGATGACATGGGGGACCTGGTGGTGCTGAGGACTATCTGGTACCCCAGCAGGC 3087
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predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArg 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen-presenting cell; immunogenic; immune response; HER-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
                                                                                                                                   Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
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/product= "HER-2/neu protein"
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                                                         to treat prostate, prostate/breast PSM, FGF8b and Her2, respectively.
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useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/neu protein (also known as p185 or c-erbB2).
                                                                                                                                                                                                                                                                                                The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (31, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The
                                                                                                                                                                                                                                                                                                                                         GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; profesoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.
                                                                                                       Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
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method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dSRNAI) that has a double-stranded
                                                                                                                                                                                                                                                                                                                                                                                              1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
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                                                                                                                                                                      Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
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(ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, particularly oncogenes, or genes expressed in pathogenic organisms (particularly plasamodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX0936-ABX10075 represent gene fragments used to illustrate the method of the invention.
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/product= "Human HER2 protein"
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P-PSDB; AAE26349.
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(KING/) KING K.
(SCHW/) SCHWALL R.
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Best Local Similarity:
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                                                                                                      The invention relates to a transgenic non-human mammal that produces in its mammary gland cells detectable levels of a native human HER2 protein or its fragment. The transgenic animals are useful as tumour models for testing HER2-directed cancer therapies, and for identifying anticancer agents. The animals may also be used as source of cells which can be immortalised in culture, in screening for compounds that have potential as prophylactic or therapeutic treatments of diseases or disorders involving expression of HER2. The anti-cancer molecules are useful for inducing apoptosis or cell death of cancer cells. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New transgenic non-human mammal that produces detectable levels of a native human HER2 protein in its mammary gland cells, useful as tumor models for testing HER2-directed cancer therapies, and for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune response; T-helper cell epitope; chitosan; CTL response; vaccine; prostate cancer; breast cancer; Her2 antigen; cytostatic; immunostimulant; gene; ds.
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26-OCT-2001; 2001WO-DK00705

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The invention relates to a method for inducing or enhancing an immune response against a polypeptide antigen in an animal, including human. The method comprises administering the polypeptide antigen or at least one variant which includes at least one first Thelper cell epitope that is foreign to the animal (foreign TH epitope) and is formulated with immunogenic. The Joypeptide antigen is weakly immunogenic or nonimmunogenic. The invention is used as vaccine. The chitosan and polypeptide antigen or its variant are useful in the preparation of an immunogenic composition for inducing or enhancing an immune response, particularly CIL response, against the polypeptide or protein antigen. The method for inducing cancer, e.g. prostate or breast cancer. The treating or ameliarating cancer, e.g. prostate or breast cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing or enhancing an immune response against an antigen, particularly cytotoxic T-lymphocyte responses, for treating or ameliorating prostate or breast cancer, comprises administering the
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Job time : 61.0384 secs
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03-NOV-2000; 2000US-245166P.
18-JUN-2001; 2001DK-0000936.
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P-PSDB; AAE26366.
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326
1 QNEDLGPASPLDSTFYRSLL.....GFFCPDPAPGAGGMVHHRHR
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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AX384609 AX384609 AX384609 Homo sap Homo sap Homo sap Homo sap Bukaryot Mammalia Hand-2im Mcneill, Confixa C e AX384607 Scores:		nomo sapie Eukaryota; Mammalia; E 1	Hand-Zimme Mcneill, P. Compositio her-2/neu- Patent: WO	COKIAA COK 1 1 3 376 a	₩.	x AX384609				AX384607 Sequence 4 f AX384607 AX384607.11 Homo sapiens Homo sapiens Eukaryota; M Mammalia; Eu Hand-Zimmerm Moneill,P.D. Compositions her "Apriens" Patent: WO 0 CORIXA CORPO	1 381 a
AX384609 LOCUGS DEFINITION Sequence ACCESSION AX384609 KEYWORDS SOURCE AUTHORS Homo sapi ORGANISM Homo sapi Editaryoti Mammalia, Homo sapi COMPOSITI TITLE COMPOSITI AUTHORS Hand-Zimm Mammalia, Morialli, Editaryoti BASE COUNT STORY CORIXA CG FEATURES SOURCE SOURCE ORGANICA OY A1140MENTICA OY 1 GINASP ON COCCIS ON COCCI ON COCCIS ON COCCI ON COC		-		o o	ignment Scred. No.: Store: Store Simi	5 (1-59)		10	1	7 5	source COUNT

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Hand-Zimmermann, S., Cheever, M.A., Foy, T.M., Lodes, M.J., Kalos, M.D., Mcneill, P.D. and Vedvick, T.S.
Compositions and methods for the therapy and diagnosis of her-Z/neu-associated malignancies
her-Z/neu-associated malignancies
Patent: WO 0214503-A 7 21-FEB-2002;
CORIXA CORPORATION (US)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidaė; Homo.
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                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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American Foundation for Biological Research Inc. (US); Mincheff,
Milcho S. (US); Loukinov, Dmitri I. (US); Zoubak, Serguei (US)
Location/Qualifiers
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Methods and compositions for inducing cell-mediated immune
                                                                                                                                       Mcneill, P.D. and Vedvick, T.S.

Compositions and methods for the therapy and diagnosis of her 2/neu-associated malignancies
Patent: WO 0214503-A $ 21-FEB-2002;

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Matches:
Conservative:
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Mismatches:
Indels: DNA 704 t 719 Indels: 3768 bp Sequence 1 from patent US 5869445. AR034479 AR034479.1 GI:5950084 FKGTPTAENPEYLGLDVPV" /organism="unknown" 1171 c 1119 g Location/Qualiflers 1091 g 4.29e-31 326.00 100.008 100.008 4.41e-31 326.00 100.00% 100.00% 1137 c SEQ5 (1-59) x AX505114 (1-3678) 3768 Unclassified Best Local Similarity: ಥ .159 746 . Unknown. Percent Similarity: Unknown Alignment Scores: Pred. No.: Alignment Scores: Query Match: DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM source BASE COUNT ORIGIN BASE COUNT ORIGIN .. 9 AUTHORS TITLE JOURNAL RESULT 6 AR034479 LOCUS REFERENCE FEATURES

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Methods of treatment using anti-erbb antibody-maytansinoid
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Sequence 2 from Patent W00100244.
AX060704 GI:12406101
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Sequence 1 from Patent WO0153463.
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/note="unnamed protein product"
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Sequence 9 from Patent W00212341.
AX380923 AX380923.1 GI:19575767
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2026. .3765
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2968. .375
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2968. .3144
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2968. .3114
//note="preferred portion of the phosphorylation domain (delta PD) of human Her-2/neu"
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                                                                                                            Her-2/neu fusion proteins
Patent: WO 0212341-A 9 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                 Cheever, M.A. and Gheysen, D.
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                                                       PAT 19-MAR-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    /note="unnamed protein product" /codon_start=1

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Methods for diagnosis and therapy of hematological and
virus-associated malignancies
Patent: WO 0213847-A 1 21-FEB-2002;
CORIXA CORPORATION (US)
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Sequence 1 from Patent W00213847.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArg 59
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Mismatches:
Indels:
Gaps:
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Novel therapeutic vaccine formulations
Patent: WO 0234287-A 3 02-MAY-2002;
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/note="unnamed protein product"
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1. 3768
1. 3768
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Sequence 3 from Patent WO0234287
AX467229
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PAT 16-AUG-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bennett, C.Frank., Lipton, A. and Witters, L.M.
Antisense oligomucleotide modulation of human HER-2 expression
Patent: US 5968748-A 1 19-OCT-1999;
                                                                                                                                                                                Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
Method for inhibiting the expression of a target gene
Patent: WO 0205693-A 52 18-JUL-2002;
Ribopharma AG (DE)
Location/Qualifiers
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758 a 1170 c 1121 g 719 t
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                                                           AX481438 3768 bp
Sequence 52 from Patent W002055693.
AX481438 AX481438.1 GI:22316352
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Sequence 1 from patent US 5968748.
AR080259
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a 1383 c 1329 g
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Homo sapiens
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AUTHORS
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                                   RESULT 13
AX481438
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AR080259
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SEQ5 (1-5	29) x	AR080259	(1-4473)			
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Qy	21 3202		AspMetGlyAspLeu 	ValAspalaGluGlu 	GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 	1111 1111 3GGC 3261
Qy Db	41		ProAspProAlaPro 	GlyalaGlyGlyMet 	PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArg 	9 59 3318
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SOURCE ORGANISM		Unknown. Unknown. Unclassified	Ţ.			
REFERENCE AUTHORS TITLE JOURNAL FEATURES	e e	Kipps, T.J. and Wu, Y. Vaccines with enhanc Patent: US 6287569-A	Kipps, T.J. and Wu, Y. Vaccines With enhanced intracellular Patent: US 6287569-A 26 11-SEP-2001; Location/Qualifiers 1. 4473		processing	
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SEQ5 (1-5	x (69	AR167390	(1-4473)			
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qa	3142		GACTTGGGCCCAGCC	AGTCCCTTGGACAGC	CAGAATGAGGACTTGGGCCCCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTG	CTG 3201
Oy Dp	21 3202		aspmetGlyaspLeu 	ValAspalaGluGlu' 	GluaspaspaspmetGlyaspLeuValaspalaGluGluTyrLeuValproGlnGlnGlnGl 	IG1y 40 GGC 3261
 ٥y	41		ProAspProAlaPro	GlyAlaGlyGlyMet	PhePheCysProAspProAlaProGlyAlaGlyGlyWetValHisHtsArgHisArg	59
qq	3262		CCAGACCCTGCCCCG	GGCGCTGGGGGCATG	GTCCACCACAGGCACCGC	3318
Search co Job time	mple: 85:	Search completed: October Job time : 855.833 secs	16, 2003,	11:03:09		

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Result October 15, 2003, 22:47:19 ; Search time 2081.84 Seconds (without alignments) 3105.423 Million cell updates/sec QNEDLGPASPLDSTFYRSLL......TFKGTPTAENPEYLGLDVPV 266 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. nucleic search, using frame_plus_p2n model 22781392 seqs, 12152238056 residues hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries BLOSUM62 Xgapop 10.0 , Ygapext (Ygapop 10.0 , Ygapext (Fgapop 6.0 , Fgapext Delop 6.0 , Delext Minimum DB seq length: 0 Maximum DB seq length: 200000000 of Perfect score: Sequence: Scoring table: Total number OM protein Searched: Run on:

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885 bp mRNA linear EST 12-NOV-2002 AGENCOURT_10735919 MAPCL Homo sapiens cDNA clone IMAGE:6722585 5', CA455074

CA455074.1 GI:24905427 Homo sapiens (human)

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 885)

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Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
linest size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.

Manuscript submitted 149 t
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristla. A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llni.gov
Plate: LLAM14285 row: i column: 17
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Ubases 1 to 4715)
Huang,Y., Zhou,X.M., Zhang,P.P., Jiang,H.Q., Qin,W.X., Zhao,X.T.,
Wan,D.F. and Gu,J.R.
Direct Submission
Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related
Genes, Shanghal Cancer Institute, 25/In 2200 Xie-Tu Road, Shanghai
200032, P. R. China
Location/Qualifiers
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21 ProProAlaPheSerProAlaPheAspAsnLeuTyr' 	rTyrTrpaspGlnaspProProGlu 240
1 ArgGlyAlaProProSerThrPheLysGlyThrPro 	oSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260
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Directionally cloned: Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted"

302 c 261 g 155 t Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14285 row: I column: 23
High quality sequence stop: 682. 186 246 306 40 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 893) NIH-WGC http://mgc.nci.nih.gov/. 21 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly Conservative: Mismatches: Indels: Gaps: Length: Matches: CA455141 GI:24905561 7.21e-78 1399.50 98.13% 97.75% Homo sapiens (human) SEQ4 (1-266) x CA455141 (1-893) Homo sapiens Unpublished Percent Similarity: Best Local Similarity: 175 Alignment Scores: Query Match: VERSION KEYWÖRDS SOURCE ORGANISM source .. Q REFERENCE AUTHORS TITLE JOURNAL COMMENT BASE COUNT ACCESSION FEATURES ORIGIN Pred. Ω ολ ŏ g ò qq õ Q

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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMA14275 row: k column: 16
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                                         ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Vector: DCMV-SPORT6; Site_1: BCORV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dr. Average insert size: 1800. bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted. The strausberg is 151 the strausberg is 151 the strausberg is 151 the strausberg in 151 the strausberg is 151 the stra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 CAGAATGAGGCCTTGGCCCAGCCATTGGACAGCTTCTACGTCGCTCACTGCTG
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Matches:
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Mismatches:
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93.38%
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219 TTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGGGGCATGGTCCACCACAGGCACCGCAGC
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TITLE
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                                                                                 AGENCOURT_14368652 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30395147 5', mRNA sequence.
CD515356
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NIH-WGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                    Unpublished
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute AIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: NDAM474 row: m column: 12
High quality sequence stop: 708.
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Matches:
Conservative:
Mismatches:
Indels:
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         CD515356.1 GI:31447074
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1340.00
96.95%
96.95%
92.41%
                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
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Pred. No.:
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ORIGIN
                                                                                                DEFINITION
                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                          RESULT 5
CD515356
                                                                                                                          ACCESSION
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ACENCOURT_6459871 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5575087 BM802792
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                        OProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGl
ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lound through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
Plate: LLAM12324 row: m column: 08
High quality sequence stop: 642.
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//Issue_type="embryonal carcinoma, cell line"
//Issue_type="embryonal carcinoma, cell line"
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Mismatches:
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Gaps:
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Matches:
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  Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM14278 row: n column: 19
High quality sequence stop: 693.
Location/Qualifiers
1. 871
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//clone="mARGE:6720019"
                                                                                                                                                               CA488274 871 bp mRNA linear EST 14-NOV-2002 AGENCOURT_10808010 MAPCL Homo sapiens CDNA clone IMAGE:6720019 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MAPCL"
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Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dr. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted.
296 c 252 g 144 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 ACCTICAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTGGGGTCTGGACGTGCCAGT 722
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 871)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BC023725
HC023725 I GI:23959125.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,W.L., Granifer,S., Guan,X., Gupta,J., Haghighi,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg.R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                              TyrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro
                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                                                                                                                                                               714
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Contact: MGC help desk
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1988)
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BC023725
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COMMENT
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FybyN"
/strain="FybyN"
/db_xref="taxon:10090"
/clone="IMAGE:5347334"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="Nor_CaAp_Mam6"
/lab_host="DH10B"
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McCowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortuum/LLML at: http://image.llnl.gov Series: IRAK Plate: 55 Row: 1 Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu
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AK031542

Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030449F08 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog 1, neuro/glioblastoma derived
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Arakwa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawaa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuchl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
   ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 200
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.

Nature 420, 563-573 (2002)

E (bases 1 to 3110)

Adachi, J. Aizawa K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haraka, T., Haroka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoto, H., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N., Okamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, T., Salto, R., Saltoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Taya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

N. Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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FQDLSYFQUILAVIRGRILHDGAYSITLOGLGTHSTGLBSCHFELDSGGALHRWYHLGF
VNTVPWDQLFRNPHQALLHSGNRPEEAGGLGGLVGNSICAŘGHCWGGGPTQCVNCSQF
LRGQECVEECRWWGLDREYVGGKHCLLPCHPECQPQNSSETCYGSEADQCEACAHYKD
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo, Cka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Tokohama Institute; 1-7.22 suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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//issue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
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neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="657BL/6J"
/db_xref="FANTOM_DB:6030449F08"
/db_xref="texon:10090"
/clone="6030449F08"
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/db_xref="G1:26327397"
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OAOMRILKETELRKLKVLGSGAFGTVYKGIMIPDGENVKIPVALKVLRENTSPKANKE
LLDEAYVMGVLLETELRKLKVLGSGAFGTVYKGIMIPDGENVKIPVALKVLRENTSPKANKE
LLDEAYVMGVRGSVLEBVRLHOLASTVOLVKSPNHVKINDFGLARLLDIDETEYHADGG
KVPIKWAALESILERRRFHQSDVWSYGYTVWELMTFGAKPYDGIPAREI PDLLEKGER
LPOPPICTIDVYMIMVKGWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGFSS
PMDSTFYRSLLEDDDMGELVDAEEYIVPQGFFSPDPALGTGSTAHRHRSSSARSGG
GELTLGLEPSEEEPPRSPLASSOVFDGDLAVGVTKGLQSLSPHDLSPLQRYSE
DPTLPLPPETDGYVADLAGSPOPEYWOPEVRROGDLAVGVTKGLQSLSPHDLSPLGRYSE
LSPGKNGVVKDVFAFGGAVENDEYLARGGASQPHPSPAFSPAFSDNLYYWDQNSSEQ
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Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnartne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.W., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                Euteleostomi;
Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                             Strausberg, R. Direct Submission Direct Submission Submission Submitted (03-F820) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ė
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This clone has the following problem: no 5' EST match.
Location/Qualifiers
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Sciurognathi; Muridae;
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Mismatches:
Indels:
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mRNA.
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/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5340777"
/tissue_type="Manmary tumor. Br
months old, gross tissue."
/clone_lib="NCL_CGAP_Manm3"
/lab_host="DH10B"
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926 g 748 t
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Mus musculus, clone IMAGE:5340777,
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Rodentia;
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Mammalia; Eutheria;
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21 G	625 TT 61 Se 685 TC	81 AlabroargSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 	101 LeuGlyMetGlyAlaalaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu 	121 GlnargTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla 	141 ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro	161 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 	181 ProLysThrLeuSerProGlyLysAsnGlyValValValLysAspValPheAlaPheGlyGly 	201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaAroGlnProHisPro 	221 ProproAlaPheSerProAlaPheAspasnLeuTyrTyrTrpAspGlnAspProProGlu 	241 ArgGlyAlaProProSerThrPheLysGlyThrProThralaGluAsnProGluTyrLeu :::	261 GlyLeuAspValProVal 266 	AK031099 4323 bp mRNA linear HTC 05-DEC-MS musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404NI0 product:v-erb-b2 erythroblas:leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian), full insert sequence.		Mammalla; Butherla; Rodentia; Sciurognathi; Muridae; Murina Jammalla; Butherla; Rodentia; Sciurognathi; Muridae; Murina Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
Qy Db 1	Db 1 Oy Db 1	Qy Db 1	Oy Db 1	Oy Db	Qy Db 1	Oy Db 1	Qy Db 2	Oy Db	Qy Db 2	Qy Db 2	Qy Db 2	RESULT 11 AK031099 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE

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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itbh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Saito,T., Rabukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Ruehl,P., Lewis,S., Matuo,Y., Nikaido,I., Pesole,S., Casavant,T., Quackenbush,J., Schimil,L.M., Staubli,F., Suzuki,Rl, Tomita,M., Wagner,L., Washio,T., Schimil,L.M., Staubli,F., Suzuki,Rl, Tomita,M., Baldarelli,R., Barsh,G., Balake,J., Boffelli,D., Bojunga,N., Andono,H., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,B., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-Oka,K., Wangy,K.H., Weltz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Recently, Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotenni, K., Ishii, Y., Itoh, M., Kagawa, T., Kavai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Sakai, C., Sakai, K., Shiraki, T., Takaku, A., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

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                                                                                                                                                                                   genes
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                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
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cDNA library was prepared and sequenced in Mouse Genome

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                                                                                                               /mol_type="mRNA"
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/strain="c57BL/6J"
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/db_xref="t4040N10"
/clone="593040N10"
/tissue_type="forelimb"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                v-erb-bz erythroblastic leukemia viral oncogene homolog
neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
match=449)"
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                                   prepare mouse tissues.
Please visit our web site for further details.
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                                                                                                                                                                                                /dev_stage="13 days embryo"
48. .3818
                                                      URL:http://genome.gsc.riken.go.jp/
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Location/Qualifiers

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    organism="Mus musculus"

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Mus musculus 9 days embryo whole body CDNA, RIKEN full-length enriched library, clone:D030063B12 product:v-erb-b2 erythroblastic lenkemia viral oncogene homolog 2, neuro/glioblastoma derived AK083669
AK083669 AK083669 Gavian), full insert sequence.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                       181 ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly
                                                   CCCAAGACTCTCTCTCTGGGAAAAATGGGGTTGTCAAAGACGTTTTTGCCTTTTGGGGGT
                                                                                                       AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Haramoto,K., Hiramoto,T., Hirozane,T., Ratoki,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kowda,M., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kowda,M., Koya,S., Kurihara,C., Matsuyama,T., Myazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Salto,R., Saltoh,H., Sakai,K., Sano,H., Yomaru,A., Tomaru,A., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y., Tomaru,A., Toya,T., Yasunishi,A., Direct Submission

AL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SSC), Ranagawa 230-0045, Japan (E-mail:genome-res@gor.riken.go.jp,, Ranagawa 230-0045, Japan (E-mail:genome-res@gor.riken.go.jp,, Prax:81-45-503-9222, Prax. Ranagawa 230-0045, Japan (E-mail:genome-res@gor.riken.go.jp,, Prax:81-45-503-9222, Prax. Ranagawa 230-0045, Japan (E-mail:genome-res@gor.riken.go.jp,, Prax. Ranagawa 230-0045, Japan (E-m
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., and Hayashizaki, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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//note="v-erb-b2 erythroblastic leukemia viral oncogene
homolog 2, neuro/glioblastoma derived oncogene homolog
(avian) (MGDIMGI:95410, GBIU71126, evidence: BLASIN, 998,
                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                            3160 GAGGATGATGACATGGGGGAGCTGGTCGATGCTGAAGAGTACCTGGTACCCCAGCAGGGA
                                                                                                                                                                           3700 GCTGTGGAGAACCCTGAATACTTAGCACCCAGAGCAGGCACTGCCTCTCTCAGCCCCACCCT
GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
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                                                                                                                                                       41 PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer
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(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is a destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."
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                            Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM492 row: j column: 17
High quality sequence stop: 662.
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Unpublished
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237
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8
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Matches:
Conservative:
Mismatches:
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932 bp mRNA linear EST 14-NOV-2002
AGENCOURT_10808060 MAPCL Homo sapiens cDNA clone IMAGE:6719711 5',
MRNA sequence.
CA487981
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/clone_lib-"MAPCL"
/clone_lib-"MAPCL"
/clone_lib-"MAPCL"
/note="Vector: pcWv-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dr. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HWE1, LNCaP"
/lab_host="EMDH10B"
                                                                    180
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI4278 row: a column: 23
High quality sequence stop: 567.
                        574
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteled
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AU123871 (685 bp mRNA linear EST 01-AUG-2002 AU123871 NT2RM2 Homo sapiens cDNA clone NT2RM2001211 5', mRNA
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                                                                     GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
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84.19%
78.38%
                                                    (1-932)
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         Percent Similarity:
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Isogai, T.

HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T.)

U Upublished
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-396
Fax: 81-438-52-396
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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            Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                 Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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1. 685
1. 685
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Mismatches:
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            Eukaryota; Metazoa;
Mammalia; Eutheria;
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Db 431 Qy 161	431 CCCCTGACCTGCAGCCTGAATATGTGAACCAGCCAGATGTTCGGCCCCAGCCC 490
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Db 491	491 CCTTCGCCCCGAGAGGGCCCTCTGCCTGCTGCCTGCTGCTGCTCTCTGGAAAGG 550
Oy 181	181 ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 200
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Search completed: Octob Job time: 2095.84 secs	Search completed: October 16, 2003, 17:04:49 Job time : 2095.84 secs

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APPLICANT: Bol, David K.
APPLICANT: Carboni, Joan M.
APPLICANT: Rowley, Ronald B.
APPLICANT: Wong, Tai W.
APPLICANT: Lee, Francis Y
TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
                                                                                                                 Sequence 165, App
Sequence 116, App
Sequence 32765, A
Sequence 390, App
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2 US-10-101-510-124
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US-09-854-356-9

US-09-441-411-5

US-09-441-411-5

US-10-131-644-1

US-10-146-473-32

US-10-207-655-44

US-09-930-125-5

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PRIOR APPLICATION NUMBER: US 60/360,889
PRIOR FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10378393
Publication No. US20030182668A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 114
LENGTH: 1713
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Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Hand Zimmernan, Susan
APPLICANT: Cheever, Martin A.
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Matches:
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Indels:
Gaps:
APPLICANT: Lodes, Michael J.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Medvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR;
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MAL.
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-125-6
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Qy 141 ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro 160 Db 1366 CCCTGACCTGCACCCCCAGCCTGAATATGTGAACCAGCCAG	201 AlavalGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 4 US-09-930-125-7 Sequence 7, Application US/09930125 Sequence 7, Application US/09930125 Sequence 7, Application US/09930125 Publication No. US20020193329A1 GENERAL INFORMATION: APPLICAMY: Hand-21mmernan, Susan APPLICAMY: Cheever, Martin A. APPLICAMY: Lodes, Michael J. APPLICAMY: Modes, Michael D. APPLICAMY: Modell, Patricia D. APPLICAMY: Wordil, Patricia D. CHRENT FILING DATE: 100-14 CURRENT FILING DATE: 2001-08-14 CURRENT FILING DATE: 100-14 CURRENT FILING DATE: 100-14 CURRENT FILING DATE: 100-14 CURRENT FILING DATE: 100-14 CURRENT FILING DATE: 2001-08-14 Alignment Scores:	
b 1606 y 241 b 1666 y 261 b 1666 s ESULT 3	US-09-930-125-4 US-09-930-125-4 Sequence 4, Application US/09930125 Publication No. US20020193329A1 GENERAL INFORMATION: APPLICANT: Hand Zimmerman, Susan APPLICANT: Cheever, Martin A. APPLICANT: Colese, Michael J. APPLICANT: Kalos, Michael D. APPLICANT: Mosill, Patricia D. APPLICANT: Wodvick, Thomas S. TITLE OF INVENTION: OWPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS FILE REFERRACE: 210121.544 CURRENT APPLICATION NUMBER: US/09/930,125 CURRENT FILIC DATE OF THE THE APPLICATION NUMBER: US/09/930,125	S S. Ili	QY, 41 PhePheCysProAspProAlaProGlyAlaclyGlyMetValHisHisArgHisArgSer 60 106 TTCTTCTGCCACCCCGGCCCTGGGGCATGGTCCACCACGCACG

Pred. No.: 8.12e-118 Length: 2411 Score: 1450.00 Matches: 266 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0 DB: 12 Gaps: 0	SEQ4 (1-266) x US-10-378-393-10 (1-2411) Qy 1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 20			Db 1731 TTCTTCTGTCCAGACCCTGCCGGGGGCTGGGGCATGGTCCACCAGGCACGCAGC 1790 Qy 61 SerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGlu 80		Db 1851 GCCCCCAGGTCTCCACTGGCACGGGCTGGCTCCGATGTATTGATGGTGAC 1910 Qy 101 LeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120	Db 1911 CTGGGATGGGGCGCGCCAGGGGCTGCCCCCCCCCAGGTGGCCTCTT 1970 Qy 121 GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla 140	Db 1971 CAGCGGTACAGTGAGGACCCCACAGAGTCCCCTGCCCTCTGAGACTGATGGCTTGCC 2030 Qy 141 ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro 160		Oy 161 ProserProArgGluGlyProLeuProAlaAlaArgFroAlaGlyAlaThrLeuGluArg 180	Qy 181 ProLysThrLeuSerProGlyLysasnGlyValValLysaspValPheAlaPheGlyGly 200	Qy 201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220	Qy 221 ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu 240	Qy 241 ArgGlyAlaProProSerThrPheLysGlyThrProThralaGluAshProGluTyrLeu 260	Qy 261 GlyLeuAspValProVal 266 	RESULT 6 US-09-854-356-9 ; Sequence 9, Application US/09854356 ; Patent No. US2002177567A1 ; GENERAL INFORMATION: ; APPLICANT: Cheever, Martin A. ; APPLICANT: Gheysen, Dirk ; APPLICANT: Greysen, Dirk ; APPLICANT: Corixa Corporation
	Qy 81 AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 100	Oy 101 LeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120	7	Qy 141 ProLeuThrCysSerProGluProGluTyrValAsnGlnProAspValArgProGlnPro 160	161 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 	<pre>Qy 181 ProfysThrLeuSerFroGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 200</pre>	Qy 201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220	Oy 221 ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu 240	241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260	61	Db 1750 GGTCTGGACGTGCCAGTG 1767 RESULT 5	os-10'378'393-10' Sequence 10, Application US/10378393 Publication No. US20030182668A1 GENERAL INFORMATION:	APPLICANT: DOI, JOAN M. ; APPLICANT: Carboni, Joan M. ; APPLICANT: Rowley, Ronald B. ; APPLICANT: Wong, Tai W. shpringanm: Wong, Tai W.	TITLE OF INVENTION: TYROSINE KINASE RECEPTORS ; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS ; FILE REFERENCE: D0254 NP	CURRENT FILING DATE: 2003-03-03 PRIOR APPLICATION NUMBER: 05/360,889 PRIOR FILING DATE: 2002-03-01 PRIOR FILING DATE: 2002-03-01	4 ໝ ໝ <u>ໍ</u>

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US-09-930-125-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3768)
OTHER INFORMATION: human HER-2/neu protein
NAME/KEY: misc_feature
LOCATION: (1)..(1959)
OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2026)..(3765)
OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2968)..(3765)
OTHER INFORMATION: 1969)
OTHER INFORMATION: 1969
OTHER INFORMATION: 100 human HER-2/neu
NAME/KEY: misc_feature
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LOCATION: (2968)..(3144)
OTHER INFORMATION: preferred portion of the phosphorylation domain
OTHER INFORMATION: (delta PD) of human HER-2/neu
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
APPLICANT: SmithKline Beecham Biologicals S. A. TITLE OF INVENTION: HER-2/neu Fusion Proteins FILE REFERENCE: 0.14058-0.09810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 3768
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Sequence 1, Application US/0930125

Publication No. US2002019332941

GENERAL INFORMATION:
APPLICANT: Hand-2immerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Michael J.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Code S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121544
CURRENT FILING DATE: 2001-08-14 3567 3627 3507 3687 3027 200 220 240 20 3448 CCTTCGCCCCGAGAGGCCCTCTGCCTGCTGCTGCTGCTGGTGCCACTCTGGAAAGG ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 181 ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 3508 CCCAAGACTCTCTCCCCAGGAAGAATGGGGTCGTCAAAGACGTTTTTGCCTTTGGGGT 2968 CAGAATGAGGACTTGGGCCCAGCCCATCCTTGGACAGCACCTTCTACCGCTCACTGCTG 1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 3768 266 0 0 0 Conservative: Mismatches: Length: Matches: Indels: CURKENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25.
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1 Gaps: (1-266) x US-09-930-125-1 (1-3768) 1.28e-117 1450.00 100.00% 100.00% 100.00%

PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer 60	8 TCATCTACCAGGAGTGGCGGTGGGGACCTGACACTAGGGCTGGAGCCCTCTGAAGAGGA 1 AlaProArgSerProLeualaProSerGluGlyAlaGlySerAspValPheAspGlyAs 1	01 LeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120 	11 GlnargfyrSerGluaspProThrValProLeuProSerGluThraspGlyTyrValala 140 	н ю	1 ProSerbroargGluGlyProLeuProalaAlaargProalaGlyAlaThrLeuGluArg 180 	11 ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 200 	11 AlavalGluAsnProGluTyrLeuThrProGlnGlyGlyAlaalaProGlnProHisPro 220 	11 ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu 240 	AigGlyAlaProProSèrThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260 	- ~	RESULT 8 US-10-313-644-1 Sequence 1, Application US/10313644 PUDLicatLon No. US20030157119A1 GENERAL INFORMATION: APPLICANT: Cheever, Martin A. APPLICANT: Hand-zimmerman, Susan TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES FILE REFERENCE: 210121.483C3 CURRENT APPLICATION NUMBER: US/10/313,644 CURRENT FILING DATE: 2002-12-04 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 3.0 LENGTH: 3768 TYPE: DNA ORGANIEM: Homo sapien FEATURE: NAME/REST: CDS USATION: (1)(3765)
30	Db 314 Qy 8 Db 320	Qy 10 Db 326	Qy 12 Db 332	Qy 14. Db 338.	Qy 16 Db 344	Qy 18: Db .3508	Qy 201 Db 3568	Qy 221 Db 3628	Qy 24.	Qy 261 Db 3748	RESULT 8 US-10-313-644-1 Sequence 1, A Sequence 1, A SEDNEAL INFORM APPLICANT: APPLICANT: TITLE OF INV TITLE

Alignment Scores:

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Length:
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APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
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Matches:
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TITLE OF INVENTION: EXPRESSION PROFILES AN
FILE REFERENCE: 1517,0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
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                                                                                  Sequence 81, Application US/10101510 Publication No. US20030148295A1 GENERAL INFORMATION:
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                      NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                  APPLICANT: WAN, JACKSON APPLICANT: WANG, YIXIN
                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-10-101-510-81
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Best Local Similarity:
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APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SUBRACE RECEPTOR ANTIGEN VACCINES
TITLE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                               Length:
Matches:
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Mismatches:
Indels:
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                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5
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Best Local Similarity:
                                                                                  LENGTH: 4473
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181 ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 200	Db 3382 GCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGCTGGCTCCGATGTATTGATGGTGAC 3441
CAGAG	3502 CACCOGARCAGIOGACCCCACACAGIACCCITICAGACCITGAGACITACCITICACCITACAGIACCITACCCTACAGIACCTACAGIACCCCAGACCTACAGIACCCCCAGACCCCCAGACCAGA
CGGGGGGCTCCACCACCACCACCACCACCACCAGAGAACCCAGAGAACCCAGAGTACCTG 3921 GlyLeuaspValproVal 266	Oy 161 ProSerProArgGluGlyProLeuBroAlaAlaArgProAlaGlyAlaThrLeuGluArg 180
cardcadra 3939	Qy 181 ProLysThrLeuSerProGlyLysAsnGlyValValValLysAspValPhèAlaPheGlyGly 200
10.40.47.3.2 Sequence 32, Application US/10146473 Publication No. US20030108888A1 GENERAL INFORMATION:	Qy 201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220
Scantar, Matchew Gout, Ivan Stockert, Elisabeth Gure, Ali	Qy 221 ProProAlaPheSerProAlaPheAspAsnLeuTyrTrpAspGlnAspProProGlu 240
AFPLICANT: Old, ligging and series of the control o	Qy 241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAshProGluTyrLeu 260
CURRENT APPLICATION NUMBER: US/10/14b,4/3 PRIOR APPLICATION NUMBER: US 60/291,150 PRIOR FILING DATE: 2001-05-15	Qy 261 GlyLeuAspValProVal 266
SECTIONS: 82 PatentIn Version 3.0 1473 Homo sapiens 5-22	RESULT 12 US-10-207-655-44 ; Sequence 44, Application US/10207655 ; Publication No. US20030118592A1 ; GENERAL INPORMATION: APPLICANT: Ledbetter, Jeffrey A.
1.52e-117 Length: 4473 1450.00 Matches: 266 100.00% Conservative: 0 100.00% Mismatches: 0 100.00% Indels: 0 14 Gaps: 0	; APPLICANT: Hayden-Ledbetter, Martha S. ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOCLOBULIN FUSION PROTEINS ; FILE REFERENCE: 390069.4010. ; CURRENT APPLICATION NUMBER: US/10/207,655 ; CURRENT FILING DATE: 2002-07-25 ; NUMBER OF SEQ ID NOS: 426 ; SOFFWARE: PatentIn version 3.0 ; SEQ ID NO 44
(1-266) x US-10-146-473-32 (1-4473)	; LENGTH: 4473 ; TYPE: DNA ; ORGANISM: HOMO sablens
1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 20 	J-207-655-44 nment Scores:
GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40 	1.52e-117 1450.00 1arity: 100.00% imilarity: 100.00%
PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer 60 	Indels: Gaps: (1-4473)
SerSerThrargSerGlyGlyGlyGlyAspLeuThrLeuGlyLeuGlubroSerGluGluGlu 80 	Qy 1 GlnasnGluaspLeuGlyProAlaSerProLeuaspSerThrPheTyrargSerLeuLeu 20
AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 100	Qy 21 GluAspAspAspAcClyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40

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Qy 41 PhePhecysProAspPr Db 3262 TTCTTCTGTCCAGACCC Qy 61 SerSerThrargSerG1 Db 3322 TCATCTACCAGGAGTGC Qy 81 AlaProArgSerProLe Qy 81 AlaProArgSerProLe Db 3382 GCCCCCAGGTCCATCACTCCATCATCATCATCATCATCATCATCATCAT		Alia	
3322 3322 81 3382	PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer 60 	Pred. Score:	Alignment Scores: Pred. No.: Score:
3382	SerSerThrargSerGlyGlyGlyaspLeuThrLeuGlyLeuGluProSerGluGluGlu 80 	Perc Best Quer DB:	Percent Similarity Best Local Similari Query Match: DB:
3382	AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp	SEQ4	(1-266) x US-(
,		δδ	1 GlnAs
Oy 101 LeuGlyMetGlyAlaAl	LeudlywetGlyAlaAlaHjaHysGlyLeuGlnSerLeudroThrHiaAspProSerProLeu 	do yo	3188 CAGAA 21 GluAs
Qy 121 GlnArgTyrSerGluAs	GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla 140	ପ୍	3248 GAGG
Db 3502 CAGCGGTACAGTGAGG	SACCCCACAGTACCCTGGCCTCTGAGACTGATGGCTACGTTGCC 3561	ζO	41 PheP
Oy 141 ProLeuThrCysSerPr 	ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro 160 	Db Qy	3308 TTCTT 61 SerSe
Qy 161 ProSerProArgGluG	ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 180	qa	3368 TCATC
Db 3622 ccriceccceAdage	seccriciecrecrecceaccrecrecrecrecrecresaage 3681	Qy	81 AlaPı
181	ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 200	qa	
Db 3682 CCCAAGACTCTCCCC	CCAGGGAAGAATGGGGTCGTCAAAGACGTTTTTGCCTTTGGGGGT 3741	Qy	101 LeuG]
Qy 201 AlaValGluAsnProG1	AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220 	g o	3488 CTGGC 121 GlnA1
Qy 221 ProProAlaPheSerPr	roalapheaspasnLeuTyrTrpaspGlnaspproProGlu 240	qa	3548 CAGC
Db 3802 CCTCCTGCCTTCAGCCC	CCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCAGGACCCACAGAG 3861	ογ	141 ProLe
241	ArgGlyAlaProFroSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260	qa	3608 CCCC
Db 3862 CGGGGGCTCCACCCAC	NGCACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTG 3921	QY	161 Prose
Qy 261 GlyLeuAspvalProval	/al 266	qa	3668 CCTTC
Db 3922 GGTCTGGACGTGCCAGT	3rg 3939	Qy	181 ProL)
RESULT 13 HS-09-971-392-70		qq	3728 CCCA
; Sequence 70, Application US/09971392 ; Publication No. US2003013428341	709971392 141	οy	201 Alava
; GENERAL INFORMATION:	Ġ.	qa	3788 GCCG3
; APPLICANT: Pearson, Cecelia ; APPLICANT: Cocks, Benjamin	ia I. 1 G.	Qy	221 ProPr
FILE OF INVENTION: GENES REGULATED	REGULATED IN DENDRITIC CELL DIFFERENTIATION	qa	3848 CCICC
CURRENT APPLICATION NUMBER: US/09/971,	: us/09/971,392 10-03	Qy	241 ArgG1
PRIOR APPLICATION NUMBER: 60	50/237, 652 -03	qa	3908 င်င်င်
; NUMBER OF SEQ ID NOS: 260 ; SOFTWARE: PERL Program		Qy	261 GlyLe
; SEQ ID NO 70 ; LENGTH: 4606		qq	3968 GGTCT
; TYPE: DNA ; ORGANISM: Homo sapiens . RFATIDE.		RESU:	RESULT 14 US-09-930-125-5
NAME/KRY: misc_feature ; OTHER INFORMATION: Template ID: 276948.4	e ID: 276948.4	- Bu	sequence 3, Appl Publication No. C GENERAL INFORMATI

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Matches:
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Indels:
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Foy, Teresa M.
APPLICANT: Lodes, Michael J.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: WcNeill, Patricia D.
APPLICANT: Wcovick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MAL.
FILLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MAL.
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARRE: FRASEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 1806
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Sequence 5, Application US/10207498

Sequence 5, Application US/10207498

Publication No. US20030143568A1

GENERAL INFORMATION:
APPLICANT: Elizabeth Singer
APPLICANT: Raif Landgraf
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: MODULATING INTERACTERIZING
TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
FILE REFERENCE: 30448.103-US-10.
CURRENT FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: 05/308,431

PRIOR FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 3765
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Search completed: October 17, 2003, 03:54:36 Job time : 299.965 secs

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                                                                                                                                     Description
and is derived by analysis of the total score distribution
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-MODEL-FRAME-LINE AND MODEL-FRAME-LISTO2003_131912_20526/app_query.fasta_1.4685
-MODEL-GROAL_JOURNIA-GASTAD -SURFIX-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-TISTO-T
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                          nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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1 QNEDLGPASPLDSTFYRSLL.
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Delop 6.0,
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Perfect score:
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                                                                                                                            OM protein
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                                                                                                                                                                                                                                                                                                                                             Sequence:
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for calciting an immune response. The invention is useful for the leavest the patient is human leakcoyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a companient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full companient fragment so direct expression of a polypeptide in appropriate host cells. The composition is useful in propriate in appropriate post cells. The composition is useful in preferably for the immunotherapy of breast cancer and other Her-2/Neuron second sequence is human connection is useful in gene therapy. The present sequence is human connection entiton is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1066 TTCTTCTGTCCAGACCCTGCCCGGGGGCTGGGGGCATGGTCCACCACAGGCACCGCAGC 1125
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                            by cDNA for the clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated Her-2/New polypeptide composition useful for therapy prevention and diagnosis of cancer, preferably breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foy TM, Lodes MJ, Kalos MD;
                                                  HICD_native_coding_region"
/transl_except= (pos:1741..1752, aa:Leu-Glu)
/note= "CDS does not include stop codon"
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Mismatches:
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/*tag= a
/product= "Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 118-119; 129pp; English,
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                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAE20483
                                                                                                                                                                                                          WO200214503-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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Score:
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1485
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                                             1606 CCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGGAG 1665
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                                                                                                                                                                                                                                                                                            240
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                                                                       LeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120
                                                                                                                                                                                  180
                                                                                                                                                                                                                                                         220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytosťatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Human protein encoded by cDNA for the clone
HICD_CT_His_coding_region"
                                    AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp
                                                                                                                                                                                            ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspVaiArgProGlnPro
                                                                                                                                                                                  161 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg
                                                                                                                                                                                                                                                                                             ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
                                                                                                            121 GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA for the clone HICD_CT_His_coding_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    AAD32744 standard; cDNA; 1767 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001WO-US41733
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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1306 CACCGGTACAGTGACCCCCACAGTACCCCTGTGACATGATGCTTGCC 1365
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                                                                                          1486 CCCAAGACTCTCTCCCCAGGGAAGAATGGGGTCGTCAAAGACGTTTTGCCTTTGGGGGT
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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Mcneill PD, Vedvick
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P-PSDB; AAE20484.
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                                                                                                                                                                                                        invention relates to an isolated Her-2/New polypeptide composition
                                                                                                                                         Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
                                                                 Kalos MD;
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28-SEP-2000; 2000US-236428P. 21-FEB-2001; 2001US-270520P.
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P-PSDB; AAE20481.
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                                                               Hand-zimmermann S,
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leavest entired. The composition is useful for the therapy and diagnosis of cancer. The composition for the diagnosis, prevention and treatment of of numan malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The juvention is useful for stimulating a real response in a comman patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full clength gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in complement of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-comman contract in gene therapy. The
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                         1510 CCCAAGACTCTCTCCCCAGGGAAGAATGGGGGTCGTCAAAGACGTTTTTGCCTTTTGGGGGT
                                                                                 ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
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is
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breast cancer; ovary cancer; colon cancer; lung cancer;
prostate cancer; genetic immunisation; tumour; vaccine; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "nucleotides 2026-3765 (claim 1) code
HER-2/neu intracellular domain"
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                         HER-2/neu;
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This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a mailgnancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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/note= "oncogene"
//trag= "region which elicits immune response"
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                                                                                           malignancy; treatment; tumour;
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93US-0033644.
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                                  Human HER-2/neu oncogene DNA
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                                                                                                                                                            New antigen-presenting cells, useful as vaccines for eliciting or
enhancing an immune response to HER-2/neu protein, particularly useful
for treating or preventing cancer, e.g. breast cancer
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                                                                                                                                                                                                                                                                                                                                                      Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ds.
                                                         ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly
            AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro
                                                                                           ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
                                                                                                       Novel isolated Her-2/{\rm Neu} polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
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human malignancies, for stimulating and/or expanding T cells specific for patient. The invention is useful for stimulating a T cell response in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy The present sequence is human Her-2/Neu protein DNA.
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The present sequence is that of human Her-2/neu oncogene cDNA.

The cDNA encodes Her-2/neu (p185), an oncogenic self protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins.

Its overexpression exinase family of receptor-like glycoproteins.

Its overexpression proteins with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins or nucleic acid molecules. In preferred fusion proteins or nucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain of a Her-2/neu phosphorylation of Her-2/neu intracellular domain or phosphorylation domain (or its Dellapp fragment). An immune response to Her-2/neu protein is elicited or enhanced by transfering the fusion protein is elicited or enhanced by transfering the fusion protein is elicited or enhanced cells concoding the fusion protein, and delivering the transfected cells concoding the fusion protein, and delivering the transfected cells concoding the fusion protein, and delivering the transfected cells concoding the fusion protein, and delivering the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has {\rm Her}-2/neu extracellular domain fused to {\rm Her}-2/neu intracellular or
                                                                                                                                                                                                                                                                                                                                    Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; human; gene therapy; gene; ss.
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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/product= "Her-2/neu"
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                  Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
order to inhibit the development of cancer in a patient.
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              SerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the
                                                                            Human; Her-2/neu; gene; ds; cytostatic; haematological malignancy; CML; acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL; chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS; Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904
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                                                        Human Her-2/neu DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568).
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                        etc.
                                                                                                      cancer
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                                                                                           New single chain Fv polypeptide binding to C-erbB-2 antigen - for imaging or treating breast or ovarian
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Matches:
Conservative:
Mismatches:
Indels:
                                                DB;
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                                                Oppermann H,
                  CETUS ONCOLOGY CORP. CREATIVE BIOMOLECULES
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                                               Huston JS,
                                                                 WPI; 1993-272889/34.
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Best Local Similarity:
                                                                          P-PSDB; AAR39568
06-FEB-1992;
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                                                                                3688 CGGGGGCTCCACCCAGCACCTTCAAAGGACACCTACGGCAGAGAACCCAGAGTACCTG
             241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu
AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro
                                                                ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein has an inframe deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbel 2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbel-2 in a sample. Agents (e.g. antispanse oligonucleotides) which inhibit the expression of SPLICE erbs-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbs-2 are useful for reducing tumor cell proliferation and treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a SPLICE erbB-2 receptor protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4472 BP; 902 A; 1383 C; 1328 G; 859 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
                                                                                                                                                                                                                                                                                                                                                                                                       encoding the SPLICE erbB-2 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "SPLICE erbB-2
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175..3942
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seq4.rng

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Page

121 GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla 140 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220 ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu 240 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly GAGGACGATGACATGGGGGACCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGC ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 4472 266 0 0 0 Matches: Conservative: Mismatches: Indels: Length: BP standard; DNA; 4473 07e-66 1450.00 100.008 100.008 (1-4472)SEQ4 (1-266) x AAA14812 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 3262 3382 161 181 3802 61 81 201 221 21 ABQ76220 241 261 ABQ76220; .. 9 RESULT 12 ABQ76220 Score: ò g g qq g g q a ò δ ολ δ ò 셤 à 셤 유 a a g Q ò ò à ò ò ò ò

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This invention describes a novel method for generating a cellular immune response in a patient to a target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. cancerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents a DNA fragment which encodes the human tumour antigen ErbB-2 described in the method of the
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                                                        immunoden;
                                                                                                                                                                                                                                                                                                                            Generating cellular immune response in patient to target protein comprises introducing vector with nucleotide sequence encoding immunogen comprising protein processing signal into cell of patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disclosed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The information in this spec has been previously disclosed WO199845444 however this spec contained no sequence information
                                                      human; vaccine; cellular immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4473 BP; 902 A; 1383 C; 1329 G; 859 T; 0 other;
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Matches:
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                                                                  cancer; tumour; ErbB-2; ds
(first entry)
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                            antigen
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                                                      Tumour antigen;
21-OCT-2002
                          tumour
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    HER-2; c-neu; ErbB2; transmembrane receptor; tyrosine kinase activity; epidermal growth factor receptor; EGFR; HER-1; cancer; breast cancer; ovarian cancer; gastric cancer; antisense oligonucleotide; expression;
          LeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu
                                            GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla
                                                                             ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro
                                                                                                                ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
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                                                called c-neu and ErbB2, encodes a transmembrane receptor, with tyrosine kinase activity. HER-2 is related to the epidermal growth factor receptor (EGER or HER-1). Aberrant HER-2 expression is present in a wide number of cancers, especially breast, ovarian and gastric cancers. This sequence is used in the invention to design 12-25 nucleotide oligonucleotides that decrease the expression of human HER-2. The modulating the expression of human epidermal growth factor receptor. The oligonucleotides are used to treat diseases or conditions associated with HER-2, particularly hyperproliferative diseases such as cancer.
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                                         This is the human HER-2 polynucleotide sequence. The HER-2 gene also
                                                                                                                                                                      Sequence 4473 BP; 902 A; 1383 C; 1329 G; 859 T; 0 other,
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                     Examples; Page 38-39;
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ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu

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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, cartic endothelium, dermal microvascular endothelium, pulmonary artery cepithelium, prostate prochable pathelium, nammary epithelium, prostate cepithelium, renal epithelium, renal prothelium, renal epithelium, renal prothelium, renal epithelium, renal prothelium, renal cortical epithelium, renal prothelium, smooth muscle, mescala dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, pulmonary artery smooth muscle, cornic smooth muscle, mesangial cells, coronary artery smooth muscle, actric smooth muscle, uterine smooth muscle, astrocytes, cortic smooth muscle, uterine smooth muscle, notetal smooth muscle, uterine smooth muscle, notetal stromal cells, coronary artery smooth muscle, cotecoblasts or prostate stromal cells, coronary artery smooth muscle, cotecoblasts or prostate stromal cells, coronary artery smooth muscle, cotecoblasts or prostate stromal cells, coronary artery smooth muscle, cotecoblasts or prostate stromal cells, respect or a sample, determining the level of RNA expression for a sample, determining the cote and distinguishing cell types. The gene or a protein corporation profile may also be used for creating miscrearrays. The corporation profile may also be used for creating miscrearrays. The confirming cell or tissue identifications and inidentifying promising confirming cell or tissue identifications and inidentifying promising confirming cell or antifungal agents.
3802 CCTCCTGCCTTCAGCCCTTCGACAACCTCTATTACTGGGACCAGGACCACCAGGAG 3861
                                                                                       Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
                                                                241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene expression profile polynucleotide SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 274-276; 850pp; English.
                                                                                                                                                                              3922 GGTCTGGACGTGCCAGTG 3939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200274979-A2
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                                                                                       1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
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BP; 902 A; 1383 C; 1329 G; 859 T; 0 other;
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266
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                                    Conservative:
Mismatches:
Indels:
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Matches:
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                                    Percent Similarity:
Best Local Similarity:
Sequence 4473
               Alignment Scores:
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AAD38904

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
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                                                               Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
hyperprol1ferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone; gene; ss.
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Conservative:
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/*tag= a
/product= "Human Her-2 protein"
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             (first entry)
                                                                                                                                                                                                                                                                                                                                          Cowsert LM;
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Best Local Similarity:
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                                       Human Her-2 DNA.
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Search completed: October 15, 2003, 23:50:06 Job time: 277.648 secs

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AX46729 Sequence
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AX58575 Sequence
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AX587649 Sequence
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BD005474 Cellular
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X03363 Human c-erb
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AX201817 Sequence
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AX384604 Sequence
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AX384610 Sequence
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1 QNEDIGPASPLDSTFYRSLL.....TFKGTPTAENPEYLGLDVPV 266
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                              - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                     2888711 seqs, 20454813386 residues
                                                                                                                                                                                                                                                                                            Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Compositions and methods for the therapy and diagnosis of her-Z/neu-associated malignancies.
Patent: WO 0214503-A 6 21-FEB-2002;
CORIXA CORPORATION (US)
1. 1755
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        PAT 19-MAR-2002
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                                             Homo sapiens (human)
Memo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/db_xref="taxon:9606"
a 517 c 531 g 33:
AX384609 1755 bp
Sequence 6 from Patent W00214503.
                              AX384609.1 GI:19577810
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                                                                                                                                                                                                                        PAT 19-MAR-2002
                                                                                                                                                                                                                                                                                                                                 Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes/M.J., Kalos,M.D.,
Mcneill,P.D. and Vedvick,T.S.
Compositions and methods for the therapy and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1185
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
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Patent: WO 0214503-A 4 21-FEB-2002;
CORIXA CORPORATION (US)
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1. 1767
Acganism="Homo sapiens"
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a 521 c 529 g 336
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Sequence 4 from Patent WO0214503.
AX384607
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1450.00
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Best Local Similarity:
Query Match:
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realures Location/C	SEQ4 (1-266) x AX384610 (1-1773)
S Cheever, M Methods f L Patent: U	Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0
SOURCE Unknown. ORGANISM Unknown. Unclassified.	7.47e-54 Length: 1450.00 Matches:
GI:5	BASE COUNT 383 a 528 c 530 g 332 t ORIGIN
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RESULT 4	source 1. 1773
1750 GGTCTGGACGTGCCAG	-1
Qy 261 GlyLeuAspValProV	Compos her-2,
	RS Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes,M.J., Mcneill,P.D. and Vedvick,T.S.
241	Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Qy 221 ProProAlaPheSerP	-
Db 1570 GCCGTGGAGAACCCCG	
Qy 201 AlaValGluAsnProG	LOCUS AX384610 1773 bp DNA linear PAT 19-MAR-2002 DEFINITION Sequence 7 from Patent W00214503.
1	T 3 610
DD 1430 CCITCGCCCCGAGAGG	Db 1726 GGTCTGGACGTGCCAGTG 1743
•	Oy 261 GlyLeuAspValProVal 266
1390	
Qy 141 ProLeuThrCysSerP	241 Ard(lvalaDroCarThrDha[vec]vThrDroThralac]asnDroClvTurla
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Db 1270 CTGGGAATGGGGCCAG	1546 GCGGTGGAGAACCCCGAGTACTTGACCCCAGGGAGGAGCTCCCCTCAGCCCCTCT
Qy 101 LeuGlyMetGlyAlaAl	201 alavalcinterconnocentationocentorical entrangement of the second control of the seco
	Oy 181 ProLysThrLeuSerFroGlyLysAsnGlyValValValValPheAlaPheGlyGly 200 11
81	Db 1426 CCTTCGCCCCGAGAGGCCCTCTGCCTGCCGACCTGCTGCTGCTCTGGAAAGG 1485
Qy 61 SerSerThrArgSerG 	Oy 161 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 180
1090	1366 CCCTGACCTGCAGCCCCCAGCCTGAATATGTGAACCAGCCAG
Qy 41 PhePheCysProAspP	141 Profesional processor of the process
	Oy 121 GINAGTYrSerGinAspProThrValProLeuProSerGiuThrAspGiyyvValAla 140
Qy 21 GluAspAspMetG	1246
Db 970 CAGAATGAGGACTTGGC	

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1569
ProAlaProGlyAlaClyGlyMetValHisHisArgHisArgSer 60
                                                                                       SlutyrLeuthrProGlnGlyGlyAlaalaaProGlnProHisPro 220
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                                                                                                                                                                                                                                                                       AlaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120
                                                                                                                                                                                AspProThrValProLeuProSerGluThrAspGlyTyrValAla 140
                                                                                                                                                                                                              ProGlnProGluTyrValAsnGlnProAspValArgProGlnPro 160
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Disis,M.L.
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1119 g 719 t
Length: 3768 Matches: 266 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0
GlnàsnGluàspLeuGlybroalaSerProLeuàspSerThrPheTyrargSerLeuLeu 20
GluaspaspaspatglyaspLeuValaspalaGluGlufyrLeuValProGlnGlnGly 40
PhepheCysProAspFroAlaProGlyAlaGlyGlymetValHisHisArgHisArgSer 60
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AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 100
LeuGlyMetGlyAlaalalysGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120
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ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro 160
ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 180
AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaAroGlnProHisPro 220
ProproalapheSerProalaPheAspAsnLeuTyrTyrTrpAspGlnAspProproGlu 240
ArgdlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260
GlyLeuAspValProVal 266
3768 bp DNA linear PAT 30-AUG-2001 from Patent WO0153463.

ryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; alia; Eutheria; Primates; Catarrhini; Hominidge; Homo. ver, M.A. and Hand-Zimmermann, S.

counds and methods for prevention and treatment of her-2/ neucoisted malignancies
mit: WO 0153463-A 1 26-JUL-2001;
XA CORPORATION (US) 3768 266 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: /note="unnamed protein product" 1. 3768
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/db_xref="taxon:9606"
1. 3768 Location/Qualifiers 1817 1817.1 GI:15391666 1.42e-53 1450.00 100.008 100.008 sapiens (human) K201817 (1-3768) sapiens .ty: .arity:

SKPCARVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSIAFLHVGAYSLTLOGGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGG	Alignment Scores: 1.42e-53 Length: 3768 Score: 1450.00 Matches: 266 Score: 1450.00 Conservative: 0 Best Local Similarity: 100.00% Conservative: 0 Ouery Match: 100.00% Indels: 0 DB: 6	(1-266) x AX380923 1 GlnAsnGluA 2968 CAGAATGAGG 21 GlUASPASPA 3028 GAGGACGATG 41 PhePheCysP 41 PhePheCysP 41 PhePheCysP 61 SerSerThrA 3148 TCATCTACCAGG 61 LeuGlyMetG 61 LeuGlyMetG 62 CCCCAGGATGG 63 CCCCCAGGATGG 63 CCCCCAGGATGG 64 CATGGCCCC 65 CCCTGACCT 66 CCCTCGCTACCAGGATGG 66 CCCTCGGATGG 67 CCCTCGCTACCAGGATGG 68 CACCTGACCT 68 CCCTCGCTACCCCCCAGGATGG 69 CCCTCGCTACCCCCCCCCCAGGATGG 60 CCCTCGCTACCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
81 AlaProArg SerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp	3568 3628 3688 3688	8-MAR-20 eostom1; . LPASPETH QVPLQRLR GGGVLIQRN GGGVLIQRN GGGVLIQRN GGGVLIQRN GGGVLIGRN GGGT GGGT GGGT GGGT GGGT GGGT GGGT G

200	Score	240	3687 QY 1	rrLeu 260 Db 2968	Accre 3747 QY 21	30	Oy 41	DD 3088 PAT 19-MAR-2002 0y 61	-1 Db 31	O _Y 81	ostomi; Db 3	. Qy 101	Kalos, M.D., Db 3268	Qy 121	Db 3328	Qy 141	3388 Db 3388	QY , 161	Db 3448	Qy 181	PASPETHLD Db 3508	ò		2 6	ν.	REDECVGEG Db 3628	CFPDEEGACQ Qy 241	rgtvykgiwi Db 3688	ASSESSMENT OF 261	MASSICATION STAR			RESULT AX46545	RESULT AX46545
181 ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly 		221 ProproAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu		241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu	3688 CGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGT	GlyLeuAspValProVal	3/48 GGTCTGGACGTGCCAGTG 3/65	3768 bp DNA linear	Sequence 1 from Patent WO0214503. AX384604.1 GT.19577806	6	Sapiens Sapiens Yota; Metazoa; Chordata; Craniata; Vertebrata;	arrhin	<pre>Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes,M.J., R Mcneill,P.D. and Vedvick,T.S.</pre>	Compositions and methods for the therapy and diagnosis of her-2/new-associated malignancies	net fine associated mailynaties Cobits Cobposition in 11-FEB-2002;			/moi_rype_ genomic DNA /db_rref="taxon:9606" 1 376	15/08 // inte-"unnamed protein product" //odo.	/couon_stat t-1 /protein_id="CAD28577.1" /aboef=nrt-10f=nr	/db_xrei="61:193//80/" /translation="MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLD	MLRHLYGGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIV RGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLJORNPO	LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGES VCAGGCARCKGPLPTDCCHEOCAAGCTGPKHSDCLACLHFNHSGTORT	DTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHVQEVTE	SNECARVCIGLOMEHLEEVRATISANIQEFAGGKKIEGSLAFLEESFUGDPASNIAPL QPEQLQVFETLEETIGYLXISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLGGLGI	SWLGLKSLKELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTAN LACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVN	CQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIV PCPINCTHSCVDLDDKGCPAEORASPLTSIISAVVGILLVVVLGVVFC	RKYTMRRILGETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKĞÎWÎ PDGENVKIPVAIKVLRENTSPRANKETI DEAVWAGVGSPYVSRIJGTGITGTGITGT	QLMPYGCLLDHYRENGRLGSQDLLINGCMQIARGNYLEDVRLYHYRDLAARNVLYKSP NIUVT THOFOTA DIT IT TROPHEVUA NICKYAT KRIMAN EGIT EDDERHINGCHARGOVARMANDA	LMITERATE CONTRACTOR THE CONTRACTOR TO THE CONTRACTOR TO THE CERTIFICATION OF THE CERTIFICATION OF THE CERTIFICATION OF THE CENTRE OF THE CERTIFICATION OF THE CENTRACTOR OF T	The second secon	FCPDPAPCAGGWYHRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDG	FCDDARGACKYNYH RHENGESTER FOLLOLL STANDARGACKYN FRONT FOLLOL FOLLOL FOLLOCKYN FEDDARGACKYN FEDDA	FCPDPAPAGAGMYHTHRISSENDAGATATAGUET TRALLELUNGULULAPSEGAGSDVFDC FCPDPAPAGAGGMYHTHRISSENGGGDLTLGLEPSEERAPSEGAPSDFDG DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR
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Sequence 1 from Patent W00213847.
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                                                                       1 (bases I to 4473)
Bennett, C. Frank , Lipton, A. and Witters, L.M.
Antisense Oligonucleotide modulation of human HER-2 expression
Patent: US 5968748 A 1 19-0cT-1999;
Location/Qualifiers
                                          LeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuProThrHisAspProSerProLeu
                                                                                                                                                            141 ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro
                                                                                                                                                                                                                      ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg
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AR080259
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                                                                                     Gaiger,A., Cheever,M.A. and Hand-Zimmermann,S.
Methods for diagnosis and therapy of hematological and
                                          Craniata; Vertebrata; E
Catarrhini; Hominidae;
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Matches:
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                                                                                                                              Patent: WO 0213847-A 1 21-FEB-2002;
CORIXA CORPORATION (US)
                                          Chordata;
Primates;
                                                                                                                virus-associated malignancies
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                sapiens (human)
                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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             Homo sapiens
Homo sapiens
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Qy	21 GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly 40	
Dp 3	3202 GAGGACGATGACGACCTGGAGGACTGAGGAGTATCTGGTACCCAGCAGGC 3261	
δy	41 PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer 60	
Dp 3	3262 TTCTTCTGTCCAGACCCTGCGGGGGCTGGGGGGGCATGGTCCACCACAGGCACCGCAGG 3321	
Qy	61 SerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGlu 80	
Dp 3	3322 TCATCTACCAGGAGTGGCGGTGGGGGACCTGACGCTTGGGCTCGAGCCCTCTGAAGAGGAG 3381	_
Οy	81 AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 100	
Dp 3	3382 GCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGCTGGGTCGTGTTTTGATGGTGAC 3441	
Qy	101 LeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120	
Dp 3	3442 CTGGGAATGGGGGCAGCCAAGGGCTGCAAAGCCTCCCAACACATGACCCCAGCCCTCTA 3501,	
,	GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla	
m	3502 CAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTTGCC 3561	
•	ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro	
gn Gn	3562 CCCCTGACCTGCAGCCCCAGCCTGAATATGTGAACCAGCCAG	
Qy	161 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 180	
Dp 3	3622 CCTTCGCCCCGAGAGGGCCCTCTGCCTGCTGCTGGTGCTGGTGCCTTGGAAGG 3681	
Qy	181 ProLysThrLeuSerProGlyLysAsnGlyValValValLysAspValPheAlaPheGlyGly 200	
Dp 3	3682 CCCAAGACTCTCTCCCCAGGAAGAATGGGGTCGTCAAAGACGTTTTTGCCTTTGGGGGT 3741	
οy	201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro 220	
Db 3	3742 GCCGTGGAGAACCCCGAGTACTTGACACCCCAGGGAGGAGCTGCCCCTCAGCCCCACCT 3801	
Qy	221 ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu 240	
Db 3		
Qy	241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260	
op 3	3862 CGGGGGGCTCCACCCAGCCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTG 3921	
οy	261 GlyLeuAspValProVal 266 .	
Db 3	922	
RESULT 10 AR167390 LOCUS DEFILITION ACCESSION VERSTON KEYWORS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE SOURCE BASE COUNT ORIGIN	10 AR167390 AR2 Conclassified. AR2 AR2 AR3 AR4 AR4 AR4 AR4 AR4 AR4 AR4	

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                                               101 LeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu
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Human c-erb-B-2 mRNA.

K03363.

G1:31197
cell surface glycoprotein; cellular oncogene; erB-2 cellular; glycoprotein; growth factor receptor; kinase; neu cellular
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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2353. .3132
/note="aa 727-986, seq. homologous to EGF receptor kinase
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/note="pot. glycosylation site"
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/note="put. polyA signal"
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                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                  Eukaryotzu, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I. (bases 1 to 4473).
Yamamoto, T., Ikawa, S., Akiyama, T., Semba, K., Nomura, N.,
Miyajima, N., Saito, T. and Toyoshima, K.
Similarity of protein encoded by the human c-erb-B-2 gene
epidermal growth factor receptor
Nature 319 (6050), 230-234 (1986)
                                                                                                                                                                                                                                                              Papewalis, J., Nikitin, A.Yu. and Rajewsky, M.F.
G to A polymorphism at amino acid codon 655 of the human
erbB-2/HER2 gene
Nucleic Acids Res. 19 (19), 5452 (1991)
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/product="put. c-erb-B-2 protein (aa 1-1234)"
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oncogene; transmembrane protein; tyrosine kinase
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/note="pot. glycosylation site"
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/protein_id=="CAA27060.1"
/db_xref="G1:31198"
/db_xref="SWISS-PROT:P04626"
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    .4473
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175. .3942
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/note="pot. 9
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Hand-Zimmermann, S., Cheever, M.A., Foy, T.M., Lodes, M.J., Kalos, M.D., Moneill, P.D. and Vedvick, T.S. Compositions and methods for the therapy and diagnosis of
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                                                                                PAT 19-MAR-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0214503-A 5 21-FEB-2002;
CORIXA CORPORATION (US)
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                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                             AX384608 1806 bp
Sequence 5 from Patent WO0214503.
AX384608
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LEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL
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CTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTF
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Patent: WO 0240059-A 7 23-MAY-2002;
Patent: WO 0240059-A 7 23-MAY-2002;
American Foundation for Biological Research Inc. (US); Mincheff,
Milcho S. (US); Loudinov, Dmitri I. (US); Zoubak, Serguei (US)
Location/Qualifiers
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                                                     1483 CCTTCGCCCCGAGAGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCACTCTGGAAAGG
 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mincheff,M.S., Loukinov,D.I. and Zoubak,S.
Methods.and compositions for inducing cell-mediated immune
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Sequence 7 from Patent WO0240059.
AX505114
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AUTHORS
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	GYVKDVFRFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPP FKGTPTAENPEYLGLDVPV" 746 a 1137 c 1091 g 704 t	cores: 3.04e-53 Length: 1442.00 Matches: ilarity: 99.62% Conservative:	Similarity: 99.62% Mismatches: : 99.45% Indels: 6 Gaps:	-266) x AX505114 (1-367	1 GlnasnGluaspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 20	21 GluaspaspaspaspmetGlyaspleuValaspalaGluGluTyrLeuValbroGlnGlnGlnGly 40 	PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer 60	SerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGlu 80 	AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 	LeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeu	121 GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla 14	. 141 ProLeuThrCysSerProGlnProGluTyrValasnGlnProAspValargProGlnPro 16	CCCTGACCTGCACCCCCAGCCTGAATATGTGAACCAGCCAG	ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg	ProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly	AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro	GCCGTGGAGAACCCCGAGTACTTGACACCCCAGGAGGAGGAGCTGCCCCTCAGCCCCACACCCAT	ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu	538 CCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGGAG 3	ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu	598 CGGGGGCTCCACCCAGCACCTTCAAAGGACACCTACGGCAGAGAACCCAGAGTACCTG 365	GlyLeuAspValProVal	658 GGTCTGGACGTGCCAGTG 367

RESULT 14 AX060704

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                        Erickson, S. and Schwall, R. Methods of treatment using anti-erbb antibody-maytansinoid conjugates conjugates 2 04-JAN-2001, Genentech, Inc. (US)
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Sequence 2 from Patent WO0100244
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Location/Qualifiers
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Qy	201 AlaValGluAsnProGluTyrLeuThrProGln	GlyGlyAlaAlaProGlnProHisPro 220	DB:	
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Qy	221 ProproAlaPheSerProAlaPheAspAsnLeuTyrTrpAspGlnAspProGlu	TyrTyrTrpAspGlnAspProProGlu 240	Qy	1 6
qq	3628 CCTCCTGCCTTCAGCCCAGCCTTCGACAACCTC	INTIALITIE	qa	2968 C
Qy	241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu	ProThrAlaGluAsnProGluTyrLeu 260	Οy	21 G
qq	3688 CGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTG	CCTACGCCAGAGCCCAGAGTACCTG 3747	QQ	3028 G
Qy	261 GlyLeuAspValProVal 266		Οy	41 P
qa	3748 GGTCTGGACGTGCAGTG 3765		qq	3088 T
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ACCESSION VERSION	AX467229 AX467229.1		οy	81 A.
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AUTHORS	Beier, A.M., Gautam, A. and Mouritsen, S.R. Novel therapeutic vaccine formulations	.S.R.	Qy	121 G
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	CCIGOTILMKDIFHKNNGLALTLIDT VCAGGCARCKGPLPTDCCHEQCAAGC	NRSKACHPCSPMCKGSRCWGESSEDCQSLTRT TGPKHSDCLACLHFNHSGICELHCPALVTYNT	QQ	3568 GC
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	WEGLESTICS LATING LATIN	QPECLOVE ELLEET 197 LI LAMPLOS LEDLES VECNON TRORI LENGAT SLILLOGICI. SWLCIRS LRELEGIS GGLALL HHNTHLCFVHTVPMDQLFRNPHQALLHTANRPEDECVGEG	QQ	3628 CC
	COPONGSVTCFGPEADQCVACAHYKDI	LACINDICARGHOWGFGFTUCVNCSQTERGIBE VEECKVIJGEPRET VNARHCLEPCHPE CQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVRPDLSYMPTWKFPDEEGACQ	٥٧	241 A
	PCPINCTHSCVDLDDKGCPAEQRASP RKYTMRRLLQETELVEPLTPSGAMPN	PCFINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKI RKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWI	qu	1 3688 C(
	PDGENVKIPVAIKVLRENTSPKANKE. QLMPYGCLLDHVRENRGRLGSQDLLNI	ILDEAYVMAGVGSPYVSRLLGICLTSTVQLVT WCMQIAKGMSYLEDVRLVHRDLAARNVLVKSP	QY	261 G
	NHVKITDFGLARLLDIDETEYHADGG LMTFGAKPYDGIPAREIPDLLEKGER!	NHVKLTUPFGLAKLLDIDETEYHADGGKVPIKMALESILRRRFTHQSDVWSYGVTVWE LMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFREL	qq	3748 GC
	VSEFSRMARDPQRFVVIQNEDLGPASI FCPDPAPGAGGMVHHRHRSSSTRSGGG DLGMGAAKGLOSI DHHDDSPLORVSER	VSERSRMARDPQREVVIQNEDIGPASPLDSTEYRSLLEDDDMGDLVDAEEYLVPQQGF FCPDPAPQAGGMVHHRHSSSTRSGGGDLTLGLEBESEBRARSPLAPSEGGSDVFDG TIGMGARGIGGT OFT PHINDSDIGGT SYSTED FOR THE COLDERVINDENTE	4000	0+01-0-000
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ALIGNMENTS

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13

Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404N10 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog 1, full insert sequence. HTC; CAP trapper. Mus musculus (house mouse) Mus musculus AK031099.1 GI:26082143 RESULT 1 AK031099 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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And Layra,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashkume,W., Hayashida,K., Hayatsu,M., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T., Katoh,H., Kawai,J., Kondo,S., Konno,H., Kouda,M., Namura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sakai,C., Sakai,C., Sakai,C., Sakai,K., Shinagawa,A., Shiraki,T., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Takaku-Akahira,S., Takaku-Akahira,S., Takaku,M., and Hayashizaki,Y., Toya,T., Takaku-Akahira,S., Prince to, Namura, M., Toya,T., Takaku-Akahira,S., Prince to, Namura, M., Tayaki, M., Takaku-Akahira,S., Prince to, Namura, M., Tayaki, M., Takaku-Akahira,S., Prince to, Namura, M., Tayaki, M., Takaku-Akahira,S., Prince to, Namura, M., Takaku-Akahira,S., Prince to, Namura, M., Tayaka, Taya, Tayaka,                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/db_xref="taxnom_10090"
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/clone=lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, UKL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                         Research Group in Riken
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                                                                                                   CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Encyclopedia Project of Genome Exploration Research Group in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://dentom.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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v-erb-b2 erythroblastic leukemia viral oncogene homolog
neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
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AK083669. GI:26101404 619 639 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Mus CysProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGlu GluGlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAsp Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) GluAlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArg Chordata; Craniata; Vertebrata; E Rodentia; Sciurognathi; Muridae; CGAGGCTGCCCAGCAGAGCAGAGCCAGCCCAGTGACA 2006 LysGlyCysProAlaGluGlnArgAlaSerProLeuThr

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Nature 420, 563-573 (2002)

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Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genomic Sciences Center (SSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

REX. 145-503-9216)
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//Lissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="9 days embryo"

    1. .4463
    7. note="v-erb-b2" erythroblastic leukemia viral oncogene
homolog 2, neuro/glioblastoma derived oncogene homolog
(avian) (MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
match=449)"

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Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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TITLE JOURNAL

COMMENT

FEATURES

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                                                                                   11 LeuLeuLeuAlaLeuLeuProProGlyAlaAla-----SerThrGlnValCysThrGly
                                                                                                                     355 ACAAGTAACAGGCTCACCCAACTGGGCACTTTTGAAGACCACTTTCTGAGCCTGCAGAGG
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MDVDPEGKYSTGATCVKRCPRNYVPDHGSCYRACGPDYYSPEDGITSCKCRCDGPCR
KVCNOIGIGEBENDIAINAINHFRYCTAL AGGDLHILPVARKBEDSTRTPPLDPREL
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MNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGIMGENNTLVWKYADANNVCHLCHANG
                                                                                                                                                       Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="liver"
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NLQIIRGNALYENTYALAILSNYGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMD
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receptor (MGD|MGI:95294)
                     Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Masusyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shinaqawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Rakahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Hiraoka,T., Hori;F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Matches:
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Yamanaka, I., Saito, T., Osaito, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gassterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsudo, I., Pescole, G., Quackenbush, J., Schrim, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wushizaki, Y., Schobach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wushizaki, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y., Yoshida, K., Wassaki, H., Nature, 409 (6821), 685-690 (2001)
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                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Lof 60,770 full-length cDNAs

Lof 60,8353 573 (2002)

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S Adachi, J. Alzawa, K. Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Rutuno, M., Hanagaki, T., Hara, T., Hara, T., Kono, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Toya, T., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Telima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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Direct Submission
          High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
  Hayashizaki,Y.
  and
  Carninci, P.
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Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300003K07 product:epidermal growth factor receptor,
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                               TTCAAATACTGCCACTGCCATCAGGGGGACCTTCACATCCTGCCAGTGGCCTTTAAGGGG
                                                                                                                                                                                                                                                                       GluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuProAspLeuSer
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                                                                                                                                                                   384 AspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPheGluThrLeu
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CSHRCRRRSPSDCCHNQCAAGCTGPRESDCLVCQKRQDEATCKDTCPPLMLYNPTYQ
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MNITCTGRGPDNCIQCAHYIDGHLYNWTYADANNYCHLCHANC
TYGCAGPGLGGCEVWPSGYVQWQWILKTFWI"

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кикки Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
Rax.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax.81-45-503-0016
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                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; epidermal growth factor receptor (MGD|MGI:95294) putative"
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                                                      Please visit our web site (http://genome.gsc.riken.go.jp/)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                               /db_xref="FANTOM_DB:1300003K07"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                  /clone="1300003K07"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 AlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArgValCysTyr
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                                                                                                TACGACCTTTCCTTCATAAAGACCATCCAGGAGGTGGCCGGCTATGTCCTCATTGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGGGACATCGTCCAAAACGTCTTTATGAGCAACATGTCAATGGACTTA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVCNGIGIGEFKDTLSINATNIKHFKYCTAISGDLHILPVAFKGDSFTRTPPLDPREL
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                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; epidermal growth receptor (MGD|MGI:95294) putative"
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Matches:
Conservative:
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                                                                                                                     ---TATGGGACAAACAGAACTGGGCTTAGGGAACTGCCCATGCGGAACTTACAGGAAATC
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                             GluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAspProLeuAspAsnThrTro
                                                                                                                                                       LeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeuCysTyrGlnAspThrIleLeu
                                                                                                                                                                                   704 CTGATTGGTGCTGTGCGATTCAGCAACAACCCCATCCTCTGCAATATGGATACTATCCAG
                                                                                                                                                                                                                  TrpLysAspile------PheHisLysAsnAsnGlnLeuAlaLeuThrLeuIle
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                                                                                                                                                                                                                                                 764 TGGAGGGACATCGTCCAAAACGTCTTTATGAGCAACATGTCAATGGACTTA-----
                                                                                                                                                                                                                                                                                                               815 ---CAGAGCCATCCGAGCAGTTGCCCCAAATGTGATCCAAGCTGTCCCAATGGAAGCTGC
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                                               614 GAAAACACCTATGCCTTAGCCATCCTGTCCAAC
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//OLONE_LID="LINESKi_dorsal_root_ganglion"
//OLONE_LID="Sall; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGACCGCCCCT(15)-3'. Size selected >
1' Kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluSerPheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGln
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Conservative:
Mismatches:
Indels:
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/dev_stage="adult, 36
/lab_host="DH10B"
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Best Local Similarity:
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT_8118591 Lupski_dorsal_root_ganglion Homo sapiens CDNA clone IMAGE:6180101 5', mRNA sequence.
BU150809.1 GI:22664341
BST.
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                                                                                              AAACTCTTCGGGACACCCAATCAGAAAACCAAAATCATGAACAACAGGGCTGAGAAAGAC
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                                                                                                                         CysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCysTrpGlyPro
                                                                                                                                                                               524 GlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCysValGluGlu
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                                                                    GlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgProGluAspGlu
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13562 row: f column: 06
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1. 964
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//do_xref="Laxon:9606"
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Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                             bp mRNA linear EST 20-FEB-2002
Homo sapiens cDNA clone IMAGE:5736771
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                Inductions of the contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: gapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12745 row: n column: 04

High quality sequence stop: 637.

Location/Qualifiers

Junce

Location/Qualifiers

June 1.1016

Arranisme"Homo sapiens"
alAlaArgCysProSerGlyVal---LysProAspLeuSerTyrMetPro---1leTrpL
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                          BM562913.1 GI:18809393
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LeuGlnAspIleGlnGluValGlnGlyTyrValLeuIleAlaHisAsnGlnValArgGln 93

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AU140362 AUG-2002 T57 bp mRNA linear EST 05-AUG-2002 AU140362 PLACE2 Homo sapiens cDNA clone PLACE2000402 5', mRNA
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1 (basea 1 to 757)
Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T. Yamamoto, J., Sugiyama, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y., Isogai, T.)
                                                                                         LeuIleGlnArgAsnProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePhe
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     Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Alas-52-3986
Email: genomics@hrico.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project; 5'- & Madical Science, University of Tokyo, and
Helix Research Institute of Medical Science, University of Tokyo, and
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Conservative:
Mismatches:
Indels:
Gaps:
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/tissue_type="placenta"
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Best Local Similarity:
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Radota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schrimi, L.M., Staubil, F., Youzuki, R., Tomita, M.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishihi,Y., Nakamura,S., Hazama,M., Nishina,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaquchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer Genalysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000) Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030449F08 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian), full insert sequence.

AK031542.1 GI:26327396
HTC; CAP trapper. 662 571 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. ArgGluTyrValAsnAlaArgHisCysLeuProCysHisProGluCysGlnProGlnAsn Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253 723 GCTCANTGACCTGTTTTGGACCGGANGCT 752 572 GlySerValThrCysPheGlyProGluAla 581 3110 bp Chordata; Rodentia; Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Mammalia; Eutheria; 10349636 AK031542 11042159 603 552 663 LOCUS JOURNAL MEDLINE PUBMED REFERENCE AUTHORS MEDLINE PUBMED REFERENCE ORGANISM REFERENCE AUTHORS TITLE MEDLINE PUBMED ACCESSION VERSION KEYWORDS SOURCE JOURNAL REFERENCE AUTHORS RESULT 9 AK031542 JOURNAL TITLE TITLE g δ g ò

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LRGQECVEECRWWKGLPREYVRGKHCLPCHPECQPQNSSETCYGSEADQCEACAHYKD
SSSCVARCPSGVKPDLSYMPIWKYPDEBGICQPCPINCTHSCVDLDERGCPAEQRASP
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PMDSTFRELLEDDDMGELVDAETLUPQGEFSPDPALGTGSTAHRHRSSSARSG
GELTLGLEPSEEEPPRSPLAPSEGAGSDVFDGDLAVGVTKGLQSLSPHDLSPLQRYSG
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3110)
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                                                                                                                                                                                                                                                  Genome Exploration Research
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Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref."taxon:10090"
/clone="6030449F08"
/sex="male"
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/strain="C57BL/6J"
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FEATURES

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                                                                                                                                                                                                                                                              TrpProAspSerLeuProAspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArg
                                                                                                                                                                                                                                                                                                       435 IleLeuHisAsnGlyAlaTyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGly
                                                                                                                                                                                                                                                                                                                                                  455 LeuArgSerLeuArgGluLeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeu
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26
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Mismatches:
Indels:
                                                                                        Matches:
                                                                             Length:
                                                                            5.35e-99
1339.00
90.65%
84.53%
36.91%
                                                                                                                                                     (1-653) x AK031542 (1-3110)
                                                                                                            Similarity:
                                   ø
                                  677
                                                                                                  Percent Similarity:
Best Local Similarit
                                                                    Scores:
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Homo sapiens (human)
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BE746725
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BE746725
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/note="vector: pcwort in the pc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs -remail.nih.gov
    Tissue Procurement: Kristi A.
    CDNA Library Preparation: Invitrogen Corporation
    CDNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
    http://image.llnl.gov
    Plate: LLAM14284 row: a column: 16
    High quality sequence stop: 582.
    Location/Qualifiers
    I. 808
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Gaps:
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                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Query Match:
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AUTHORS
TITLE
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BE746725 894 bp mRNA linear EST 15-SEP-2000 601579159F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927927 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Trissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
273 ThrTyrAsnThrAspThrPheGluSerMetProAsnProGluGlyArgTyrThrPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 AAGTGCAGCAAGCCCTGTGCCCGAGTGTTCTATGGTCTGGGCATGGAGCACTTGCGAGA
                                                                             233 ThraspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCys
                                                                                                                                                        253 LeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLeuHisCysProAlaLeuVal
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High quality sequence stop: 762
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
2 a 285 c 252 g 185 t
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Conservative:
Mismatches:
Indels:
Gaps:
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// organism="mans musculus"
// organism="mans musculus"
// folone="IMAGE: 6826841"
// clone="IMAGE: 6826841"
// clone="IMAGE: 6826841"
// dev_stage="wnbryo 13.5.14.5,16.5,17.5dpc"
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// clone_lib="nil" Hib_BmAk=FV0"
// clone_lib="nil" Hib_mans constructed according Site_2: Not I: The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcse gel: First strand cDNA synthesis was primed with Oligo-dry primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with ECOR I adaptor, digested with NotI and then cloned directionally into pXY-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AcCGAGACAG. This library was created for the University low Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Montal Health (NIMH), Hemin Chin, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                          EST 27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lih, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                      818
                                                                                                                                                                     525
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
TCATCACATAAAAACCCACTC-TGTTCGTGCCCCAGGTGCCCTGGGACCAGCTCTTGG-
                                                                        AsnProHisGlnAlaLeuLeuHisThrAlaAsnArgProGluAspGluCysValGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                       CA328613 17-NOV-
UI-M-FYO-cda-e-16-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone
IMAGE: 6826841 5', mRNA sequence,
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238 c 216 q
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Seq primer: pYX-5.
Location/Qualifiers
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Alignment Scores:

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1. .1201

/ Organism="Homo sapiens"

/ forganism="Homo sapiens"

/ mol_type="mkNa"

/ db xref="taxon:9606"

/ clone="CSODI032YB05"

/ tissue_type="PLACERYA COT 25-NORMALIZED"

/ clone_lib="Homo sapiens PLACERYA COT 25-NORMALIZED"

/ note="lib="Homo sapiens PLACERYA COT 25-NORMALIZED"

/ note="lib="Homo sapiens primed with a NotI-Oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMYSORT 6 vector. Library was normalized."

55 a 376 c 321 g 223 t 46 others
                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BB 191 91006 EVRY cedex - France
Ball 182 Ferral France
Ball 182 Ferral France
BB 185 F. For more Information about this cluster, see
http://www.genoscope.ors.fr
cgi-bin/cluster.cgi?seq-CslA10082H03QP1&cluster-8568.f. Contact :
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSlA1008ZH03QP1.
                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Contact: Genoscope
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BX402419 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI032YB05 5-PRIME, mRNA sequence.
BX402419
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=GV16t2=QV1-BT0260-011199-024-all&t2=1999-11-01&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 612.
Location/Qualifiers
Location/Qualifiers
1. 614
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//moltype="mkMa"
//db_xref="taxon:9606"
//dev_stage="Adult"
//dclone_lib="BYT0260"
//orce="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
//orce="Organ: breast; Vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringeness.
                                                                                      04-FEB-2000
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mRNA sequence.
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I (bases I to 614)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
Unpublished
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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BT0260 Homo sapiens cDNA,
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Conservative: Mismatches: Indels:

Length: Matches:

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seq3.rst

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Best Local Similarity:
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//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Mol_type="mRNA"
//db_xref="taxon:9606"
//clone="Inhabdomyosarcoma"
//tissue_type="rhabdomyosarcoma"
//tab_nost="bH108 (phage-resistant)"
//clone_lib="NHH_MGC_17"
//note="Organ: muscle; Vector: poTB7; Site_1: EcoRI;
Site_2: Xhoi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhoi sites using the following 5' adaptor: GGCAGGG(G). Size-selected 550bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                            AW410534 613 bp mRNA linear EST 29-JUN-2000 fh06h06.xl NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961635 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Plate: LLCM56 row: O column: 12 Plate: LLCM56 row: O column: 12 Seq primer: -21M13 forward primer (ABI).
                                          ThrAspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCys
                                                                                                   LeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLeuHisCysProAlaLeuVal
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                      575 ThrCysPheGlyProGluAlaAspGlnCysValAlaCysAlaHisTyrLysAspProPro
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                 455 LeuArgSerLeuArgGluLeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeu
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Job time : 5138.68 secs
(1-613)
SEQ3 (1-653) x AW410534
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Sequence 5, Application US/10207498
Publication No US20030143568A1
GENERAL INFORMATION:
APPLICANT: Raif Landgraf
APPLICANT: Raif Landgraf
APPLICANT: David Eisenberg
TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
FILE REPERENCE: 30448.103-US-U1
CURRENT APPLICATION NUMBER: US/10/207,498
CURRENT PILING DATE: 2002-07-29
PRIOR PETLING DATE: 2001-07-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                Sequence 119, App
Sequence 124, App
Sequence 12, App
Sequence 10, Appl
Sequence 70, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 15, Appl
Sequence 1731, Appl
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                 - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Fgapop 6.0 ,
Delop 6.0 ,
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                                                                           ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
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201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 3 ITyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 3 ITALHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	421 AspleuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440	461 LeuGlySerGlyLeuAlaLeulleHisAsnThrHisLeuCysPheValHisThrVal 480	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHiSCys 520 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHiSCys 560 [
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301 ATTGTGCGAGGCACCCAGCTCTTGAGGACAACTATGCCCTGGCCGTGCTAGACAATGGA 360 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 20 [21 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300 111111111111111111111111111111111111	321 GluvalThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340	361 IleGinGluPheAlaGlyCysLysLysLlePheGlySerLeuAlaPheLeuProGluSer 380	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420	441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
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	InargalaSerProLeuThrSer 653 	; Patent No. US20020035736A1 ; GENERAL INFORMATION: ; APPLICANT: Exideson, Sharon ; APPLICANT: Schwall, Ralph ; APPLICANT: King, Kathleen ; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL ; FILE REFERENCE: GENENT.034A ; CURRENT APPLICATION NUMBER: US/09/811,115 ; CURRENT ELLING DATE: 2001-03-16 ; PRIOR FILING DATE: 2000-03-16 ; PRIOR FILING DATE: 2000-03-16	NUMBER OF SEC 1D NOS SOFTWARE: FastSEQ for SEQ ID NO 2 LENGTH: 3768 LENGTH: 3768 TYPE: DNA ORGANISM: Homo sapiu S-09-811-115-2	milari Simila h:	1 MetGluLeuAlaAlaLe 	41 ThrHisLeuAspWetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60 11 11 11 11 11 11 11	GlnGlyTyrValLeuIlealaHisAsnGlnValargGlnValProLeuGlnArgLeuArg 10 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]

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SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
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LOCATION: (2968)..(3765)
OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
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APPLICANT: Gheever, Martin A.
APPLICANT: Gheyen, Dirk
APPLICANT: Grixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/new Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver: 2.1
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LOCATION: (1)..(3768)
OTHER INFORMATION: human HER-2/neu protein
NAME/KEY: misc_feature
LOCATION: (1)..(1959)
OTHER INFORMATION: extracellular domain (ECD)
NAME/KEY: misc_feature
LOCATION: (2026)..(3765)
OTHER INFORMATION: intracellular domain (ICD)
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; NAME/KEY: misc_feature
; LOCATION: (2968)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (delta PD) of human HER-2/neu
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Indels:
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Matches:
Conservative:
Mismatches:
Indels:
                                                    APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Ralos, Michael D.
APPLICANT: Weneill, Patricia D.
APPLICANT: Weneill, Patricia D.
APPLICANT: Venovick, Thomas S.
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MAI
FILE REFERENCE: 210121:554
CURRENT FILIATION NUMBER: US/09/930,125
CURRENT FILIATION NUMBER: 2011-08-14
NUMBER OF SEO ID NOS: 25
                                                                                                                                          ILLING DATE: 2001-08-14
SEQ ID NOS: 25
FastSEQ for Windows Version
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                              Sequence 1, Application US/09930125 Publication No. US20020193329A1 GENERAL INFORMATION:
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US-09-930-125-1
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DB:
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ORGANISM: HOMO
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	Db 1261 GACCTCAGGGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGGC 132	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	Oy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480	Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	Oy 501 GluaspGluCysValGlyGluGlyLeuAlacysHisGlnLeuCysAlaArgGlyHisCys 520	Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 111111111111111111111111111111111111	Oy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560	Oy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580	Oy 581 AlaAspGlnCysValAlaCysAlaHisTyrLySASpProPheCysValAlaArgCys 600	Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620	Oy 621 GlyAlaCySGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640	Oy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653	RESULT 7 US-09-441-411-5 ; Sequence 5, Application US/09441411 ; Publication No. US20030008342A1	; GENERAL INFORMATION: ; APPLICANT: SCholler, Nathalie B. ; APPLICANT: Disis, Mary L. ; APPLICANT: Helistrom, Ingegerd	; APPLICANT: Hellstrom, Karl Erik ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES ; FILE REFERENCE: 730033.409 ; CURRENT APPLICATION NUMBER: US/09/441,411	; CURRENT FILING DATE: 1999-11-16 ; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 5	; LEWTH: 4473 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-441-411-5	0 Length: 3628.00 Matches:	Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0
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Qy Dp	461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480 	QY	21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
oy Op	481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500 	QY Db	41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
oy Oy	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520 	QY Db	61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
oy Op	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 	ζζ	81 GlnGlyTyrValLeullealaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Qy Dp	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHiSCys 560 	ζζ	101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
cy Bp	561 LeuProCyshisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 	QY	121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
oy B	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 	Qy	141 GInLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
δ Q	601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620 	QQ	16] LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
g ç	621 GlyalacysGlnProcysProlleasnCysThrHisSerCysValaspLeuAspAspLys 640 	Qy	181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Qy	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653 	Qy	201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
RESULT 11 US-09-877-177-11 ; Sequence 11, A	SULT 11 -09-877-177-11 Sequence 11, Application US/09877177 Dublication No HS2002010255281	Qy	221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
GENERA; APPLIC; TITLE	GENERAL INFORMATION APPLICANT: Feter V. Danenberg et al. TITLE OF INVENTION: Method of determining Epidermal Growth TITLE OF INVENTION: Factor Pacastor and UPD2 Nam. Conc. Execution	Qy	241 AlaalaciycysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
FILE CORRE	FILE REFERENCE: 11220/120 CURRENT APPLICATION NUMBER: US/09/877,177 CURRENT FILING DATE: 2001-06-11	Qy	261 SerGly11eCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
SECTION 11: SECTION 11: CENCTH: 45:	SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 11 LENGTH: 4530	Qy	281 SerMetBroAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
; ORGANISM: HO US-09-877-177-11	ORGANISM: Homo sapiens 9-877-177-11	OY Db	301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Alignment Scores Pred. No.: Score: Percent Similari	Alignment Scores: 0 Length: 4530 Score: 3628.00 Matches: 653 Percent Similarity: 100.00% Conservative: 0	QY	321 GluvalThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Query Match: DB:	100.00% Indels: 10 Gaps:	Qy	341 ValcysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
SEQ3 (1-6 Qy	SEQ3 (1-653) x US-U9-877-177-11 (1-4530) Qy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20	δλ	361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380

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Publication No. US20030143539A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCIS
APPLICANT: BIRMBAUM, DANIEL
APPLICANT: BIRMBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PARRICE
APPLICANT: VIENS, PARRICE
APPLICANT: VIENS, PARRICE
APPLICANT: VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
                                           AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla
                                                                                                        TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu
                                                                                                                                      LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 119
                                                                                                FEATURE:
COTHER INFORMATION: v-erb-b2
THER INFORMATION: oncogene
COTHER INFORMATION: oncogene
US-10-007-926A-119
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
                                           641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
                                                                                                   APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND 18 TITLE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 124
LENGTH: 4530
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US-10-101-510-124
Sequence 124, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
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                                                                          SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
                                                                                                    GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
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AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis
      SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
                                IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer
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Oy	161 LeuCysTyrClnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180	Qy 521 TrpGlyProGly
QQ		Db 1711 TGGGGTCCAGGG
Qy	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	Qy 541 ValGluGluCys
qq		1//1
δy	201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220 	Db 1831 TTGCCGTGCCAC
QY	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	Oy 581 AlaAspGlnCys
QQ		1891
Οy	241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	•
QQ	871 GCTGCCGGCTGCACGGGCCCCAAGCACTGCCTGGCTGGCT	1951
QY	261 SerGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280	Oy 621 GLYALaCysGln
qa		2011
Oy to	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	8
a		14
ογ	301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeutisAsnGln 320	
qa		; Sequence 1, Application (
δλ	321 GluValThrAlaGluAspGlyThrGluArgCysGluLysCysSerLysProCysAlaArg 340	; GENERAL INFORMATION: ; APPLICANT: Genzyme Corp. ; APPLICANT: Nicolette.
q		; FITE OF INVENTION: THE
δ	341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360	CURRENT APPLICATION NUM CURBENT TITUS DATE:
අු		CONTRACT FILING DATE: FRIOR PAINTED FILING DATE: DELOB FILING DATE:
ογ	361 IleGlnGluPheAlaGlyCysLysLysLlePheClySerLeuAlaPheLeuProGluSer 380	; NUMBER OF SEQ ID NOS: 1(
q		SEQ ID NO. 1
δy	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	TYPE: DNA
qa	1291 TITGATGGGACCCAGCCTCCAACACTGCCCCGCTCCAGGCAGCAGCACCTCCAAGTGTTT 1350	
Qy	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuDro 420	HOCATION: (151)(3915
qa	1351 GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT	; OTHER INFORMATION: US-10-338-730-1
δλ	421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440	cores:
qq	1411 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGACGAATTCTGCAATGGCGCC 1470	Pred. No.: 0
Qy	441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	ilarity: Similarity:
qq	1471 TACTCGCTGACCTGCAAGGGCTGGGCATCACCTGGCGCTGGGCTGCGCTCACTCA	
Qy	461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480	SEQ3 (1-653) x US-10-338-73
Dp	1531 CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACTCTGCTTCGTGCACACGGTG 1590	Qy 1 MetGluLeuAla
δy	481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	
đ	1591 CCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGGCA 1650	Oy 21 AlaSerThrGlnV
Qy	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	Db 211 GCGAGCACCCAAG
qq	1651 GAGGACGAGTGTGGGCGAGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGGCACTGC 1710	Oy 41 ThrHisLeuAspN

Oy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540	541 ValGluGysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 56 	Qy 561_LeuProCysHisFroGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 111111111111111111111111111111111111	Oy 601 ProSerGlyValLysProAspLeuSerTyrWetProIleTrpLysPheProAspGluGlu 620	RESULT 14 US-10-338-730-1 Sequence 1, Application US/10338730 Sequence 1, Application US/10338730 Sequence 1, Application No. US20030147905A1 GENERAL INFORMATION: APPLICANT: Genzyme Corporation APPLICANT: APPLICATION APPLICANT: THERAPEUTIC COMPOUNDS FILE REPREMEE: 5017 CURRENT APPLICATION NUMBER: US/10/338,730 CURRENT FILING DATE: 2003-01-08 PRIOR APPLICATION NUMBER: US/00/336,730 SOFTWARE: PATOR DATE: 2002-03-16 NUMBER OF SEQ ID NOS: 10 SOFTWARE: PATOR NOS: 10 SEC ID NO 1 LENGTH: 4530 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (151)(3915) US-10-338-730-1	Alignment Scores: Pred. No.: Score: Score: Asserved: Percent Similarity: Query Match: 100.00% Mismatches: Query Match: 12 Gaps: O Length: 4530 Matches: 653 Conservative: Mismatches: 0 Gaps: O Conservative: Co	SEQ3 (1-653) x US-10-338-730-1 (1-4530) QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuFroProGlyAla 20
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seq3.rnpb

421 AspLeuSerValPheGlnAsnLeuGlnVallleArgGlyArglleLeuHisAsnGlyAla 440	481 ProtrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro		Db	1 GlyCys 1 GGCTGCC 3-125 25, Appl. n No. US. FORMATIO : Lillie	APPLICANT: Zhao, Xumei APPLICANT: Gannavarpu, Manjula APPLICANT: Kamatkar, Shubhangi APPLICANT: Martar, Shubhangi APPLICANT: Mertens, Maureen APPLICANT: Myer, Vic APPLICANT: Wang, Youzhen APPLICANT: Hoersch, Sebastian APPLICANT: Monahan, John APPLICANT: Monahan, John APPLICANT: Mortobagyi, Gabriel E. APPLICANT: Hortobagyi, Gabriel N. APPLICANT: Merc, Funda APPLICANT: Merc, Funda APPLICANT: Merc, Funda APPLICANT: Sahin, Aysegul APPLICANT: Mills, Gordon B. TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
ACCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCTGCAGGGAAACCTG 330		161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla		SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	1111 GAGGTGACAGGGATGGGAACAGGGGGTGTGAGAAGTGCAGGAAGGCCTGTGCCCGA 1170

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           PREVENTION, AND THERAPY
TITLE OF INVENTION: PREVENTION, AND THERAPY
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT APPLICATION NUMBER: US/00/177,293
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-09-25
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PRIOR PELING DATE: 2002-03-05
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qq	1831	TIGCCGIGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGGG 1890
Qy	581	581 AlaAspGlnCysValalaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
qa	1891	1891 GCTGACCAGTGTGTGTGTGTGTGTGTAAAGACCCCCCCTTCTGCGTGGCCCGCTGC 1950
οy	601	ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620
QQ	1951	CCCAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
ογ	621	621 GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640
qa	2011	GGGGGATGGCAGCCTTGCCCCCATCAACTGCACTCCTGTGTGGGACCTGGATGACAAG 2070
δ	641	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Dp	2071	1071 GGCTGCCCGCCGAGAGAGCCAGCCTCTGACGTCC 2109
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                                                                              Description
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and is derived by analysis of the total score distribution.
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-O-/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_15102003_131912_20526/app_query.fasta_1.4685
-O-/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_15102003_131912_20526/app_query.fasta_1.4685
-O-/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_15102003_131912_20526/app_query.fasta_1.4685
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-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTPAT-pto -NORM-ext -HARASIZE-500 -MINIEN-0 -MAXLEN-20000000
-USRS-HOLLERAN480_4CGN_1_1_1758_4Cunat_15102003_131912_20526 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6
-FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELLOP=6 -DELEXT-7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                           Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response
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breast cancer; prostate cancer; ovarian cancer; lung cancer;
colon cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuFroProGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancers, and may be used as an antigen to vaccinate against
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Matches:
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181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200	221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240	241 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrasnThrAspThrPheGlu 280	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	301 TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln 320	321 GluvalthralagluaspGlythrGlnargCysGluLysCysSerLysProCysalaarg 340	341 ValcysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360	361 IleGInGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420	421 AspleuservalpheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440	441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	461 LeuGlySerGlyLeualaLeuIleHisHisAsnThrHisLeuCySPheValHisThrVal 480	481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	521 Trp6lyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
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                   581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
                                                                                                                                                                                     541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
                                                                               561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNA encoding HER-2-new poly:peptide(s) - used for prevention or reatment of malignancies with which the HER-2/new oncogene is issociated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
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normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Ly8676-Vall255) of the HER-2/n protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellul domain in transformed host cells, or are used, alone or in a vira vector, for genetic immunisation of an animal. Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;	& <u>.</u>		MetGluLeualaalaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyala 	AlaSerThrGlnValCysThrGlyThrAspWetLySLeuArgLeuProAlaSerProGl 	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	ACCCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGGTGCAGGGAAACCT	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 	GInGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuAr 	lleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	ATTGTGGGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGCTAGACAATGGA	ASPProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 	GAGGCCTGC	olinedarysetteurintolintilleeryselyselyselyselserinegasityselsel 	LeuCysTyrGlnAspThrileLeuTrpLysAspilePheHisLysAsnAsnGlnLeuAla	AGAACAACC	Lettini beutrasprinasiargserangatacystistroogseryooderystysys 	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys		AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	GCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCTGCTGCTGCCATGAGCAGTGT	AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	GCCTCCACT	SerGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
of the calls5) or calls5) or calls5, calls5, calls6, c	376 653 ve: 0 i: 0		uLeuAlaI 	sLeuArgi 	yCysGlnV	CTGCCAGG	rPheLeuG 	gGlnValP 	rAlaLeuA	TGCCCTGG	aSerProG	To.1 Levin	yvalleul 	ePheHisL	CITCCACA	SHISPIOC	sGlnSerL	TCAGAGCC	oThraspo	CACTGACT	SLeuAlaC	CCTGGCCT	1ThrTyrA
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normal gen code for t code for t Protein, w Nucleic ac domain in vector, fo	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Ouery Match:	(1-653) x	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	21 A		121 A	61 G 181 G	81 G 241 C	101	301 A	121 A		421 C	161 1			201 G	601 6	221 A	661 G		721 6	261 S
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361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
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                                                                                                                                      GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeüGlnArgLeuArg
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MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla
                                                            21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu
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/product= "HER-2/neu"
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tumour; ss.
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malignancy; treatment;
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P-PSDB; AAW92406.
                                                                                                     AAX01912 standard;
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 05-OCT-1998;
 20-OCT-1998;
 13-APR-2000
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LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
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 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla
 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu
 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
 Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
 Human heregulin 2 (Her2) coding sequence.
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 AAA09455 standard; DNA; 3768
 (first entry)
 10-AUG-2000
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The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (1.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 B-cell group derived from the human/murine FGR8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human and the prostate of prostate/breast or breast cancer when the PA is human and the part of
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 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal
 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
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 Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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 BP; 758 A; 1170 C; 1121 G; 719
 Claim 62; Page 187-193; 220pp; English.
 Nielsen KG,
 PSM, FGF8b and Her2, respectively.
 Mouritsen S, Niels
Birk P, Karlsson G;
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99WO-DK00525
 98DK-0001261
98US-0105011
 SEQ3 (1-653) x AAA09455 (1-3768)
 (MEBI-) M & E BIOTECH AS.
 WPI; 2000-349917/30
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAY92620
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 ACTGGCCCTCATCCACCATAACACCCCTCTGCTTCGTGCACACGGTG 1440
 nProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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 ell; immunogenic; immune response; HER-2/neu; tostatic; vaccine; pl\theta5; c-erb\theta2; ds.
 aGluGlnArgAlaSerProLeuThrSer 653
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duct= "HER-2/neu protein"
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 tion/Qualifiers
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 US01850.
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New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
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Claim 1; Page 41-46; 49pp; English

The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/new protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/new protein, particularly in treating or preventing malignancies in which the HER-2/new oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/new protein (also known as pl85 or c-erbb2). 

Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;

| Alignment Sco<br>Pred. No.:<br>Score:<br>Percent Simil<br>Best Local Si<br>Query Match:<br>DB: | scores:<br>milarity:<br>Similarity:<br>.h: | 1.51e-229<br>3628.00<br>100.00%<br>100.00%<br>100.00% | Length: Matches: Conservative: Mismatches: Indels: Gaps: | 3768<br>653<br>0<br>0<br>0                                       |     |
|------------------------------------------------------------------------------------------------|--------------------------------------------|-------------------------------------------------------|----------------------------------------------------------|------------------------------------------------------------------|-----|
| SEQ3 (1-653                                                                                    | ) x AAH23392                               | (1-3768)                                              |                                                          |                                                                  |     |
| 0y                                                                                             | 1 MetGluLeu                                | AlaAlaLeuCysArg                                       | TrpGlyLeuLeuLeuA                                         | 7                                                                | 0   |
| qa                                                                                             | 1 ATGGAGCTG                                | GCGGCCTTGTGCCGC                                       | TGGGGCTCCTCCTCG                                          | ATGGAGCTGGCGGCCTTGTGTGTGTGTGTGTGTGTGTGTG                         | 0   |
| 0y                                                                                             | 21 AlaSerThr                               | GlnValCysThrGly                                       | ThrAspMetLysLeuA                                         | AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40  | o   |
| QQ                                                                                             | 61 GCGAGCACC                               | CAAGTGTGCACCGGC                                       | ACAGACATGAAGCTGC                                         |                                                                  | 120 |
| Qy                                                                                             | 41 ThrHisLeu                               | AspMetLeuArgHis                                       | LeuTyrGlnGlyCysG                                         | invalvalGinGlyAsnLeu 60                                          | 0   |
| Db 1                                                                                           | 121 ACCCACCTG                              | GACATGCTCCGCCAC                                       | CTCTACCAGGGCTGCC                                         | ACCCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGCTGCAGGGAAACCTG 180 | 80  |
| Qy                                                                                             | 61 GluLeuThr                               | TyrLeuProThrAsn                                       | AlaSerLeuSerPhel                                         | œ                                                                | 0   |
| Db 1                                                                                           | 181 GAACTCACC                              | TACCTGCCCACCAAT                                       | GCCAGCCTGTCCTTCC                                         | GAACTCACCTACCTGCCCACCAATGCCAGCTGTCCTTCCT                         | 40  |
| Qy                                                                                             | 81 GlnGlyTyr                               | ValLeuIleAlaHis                                       | AsnGlnValArgGlnV                                         | GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 10  | 100 |
| Dp 3                                                                                           | 241 CAGGGCTAC                              | GTGCTCATCGCTCAC                                       | AACCAAGTGAGGCAGG                                         |                                                                  | 300 |
| 0y 1                                                                                           | 101 IleValArg                              | GlyThrGlnLeuPhe                                       | GluAspAsnTyrAlaL                                         | IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 12  | 120 |
| Db 3                                                                                           | 301 ATTGTGCGA                              | GGCACCCAGCTCTTT                                       | GAGGACAACTATGCCC                                         |                                                                  | 360 |
| 0y 1                                                                                           | 121 AspProLeu                              | AsnAsnThrThrPro                                       | ValThrGlyAlaSerP                                         | М                                                                | 40  |
| Dp 3                                                                                           | 361 GACCCGCTG                              | AACAATACCACCCCT                                       | GTCACAGGGGCCTCCC                                         | GACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAGGAGGCCTGCGGGGAGCTG 42 | 20  |
| 0y 1                                                                                           | 141 GlnLeuArg                              | SerLeuThrGluIle                                       | LeuLysGlyGlyValL                                         | -                                                                | 09  |
| Db 4                                                                                           | 421 CAGCTTCGA                              | AGCCTCACAGAGATC                                       | TTGAAAGGAGGGGTCT                                         | CAGCITCGAAGCCTCACAGAGATCTTGAAAGGGGGTCTTGATCCAGCGGAACCCCCAG 48    | 80  |
| 0y 1                                                                                           | 161 LeuCysTyr                              | GlnAspThrIleLeu                                       | TrpLysAspIlePheH                                         | LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 18  | 80  |
| Db 4                                                                                           | 481 CTCTGCTAC                              | CAGGACACGATTTTG                                       | TGGAAGGACATCTTCC                                         | 2                                                                | 40  |
| 0y 1                                                                                           | 181 LeuThrLeu                              | IleAspThrAsnArg                                       | SerArgAlaCysHisF                                         |                                                                  | 200 |
| op qa                                                                                          | 541 CTCACACTG                              | ATAGACACCAACCGC                                       | TCTCGGGCCTGCCACC                                         | - 22                                                             | 009 |
| 0y 2                                                                                           | 201 GlySerArg                              | CysTrpGlyGluSer                                       | SerGluAspCysGlnS                                         | GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 22  | 220 |
| pp qa                                                                                          | 601 GGCTCCCGC                              | TGCTGGGGAGAGAGT                                       | TCTGAGGATTGTCAGA                                         |                                                                  | 099 |

221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240

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| qa ko      | 661 GC<br>241 A1          |                                                                       |
|------------|---------------------------|-----------------------------------------------------------------------|
| qa         | 21 G                      |                                                                       |
| රු අධ      | 261 Se<br>   <br>  781 AC | erGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280<br>   |
| Qy<br>Db   | 281 Se<br>                | erMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300<br>   |
| Qy<br>Db   | 301 Ty<br>  <br>901 TA    | yrksntyrleuserthraspvalglysercysthrleuvalcysProleuHisasngln 320<br>   |
| Qy<br>Dp   | 321 G1<br>                | luValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg   340<br> |
| . da       | 341 Va<br>  <br> 1021 GT  | alcystyrdlyLeuglyMetGluHisLeuargGluValargAlaValThrSerAlaAsn 360<br>   |
| Qy<br>Db   | 361 I1<br>  <br> 081 AT   | leGinGluPhealaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380<br>   |
| Qy<br>Db   | 381 PP<br>  <br> 141 TT   | heAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400<br>   |
| Qy<br>Db   | 401 G1<br>  <br> 201 GA   | uThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420<br>    |
| Oy<br>Db   | 421 As<br>  <br> 261 GA   | spLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440<br>   |
| Qy<br>Db   | 441 Ty<br>  <br> 321 TP   | yrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460<br>   |
| Qy<br>Db 1 | 461 Le<br>  <br> 381 CT   | euGlySerGlyLeualaLeulleHisHisAsnThrHisLeuCysPheValHisThrVal 480<br>   |
| Qy<br>Db   | 481 Pr<br>  <br> 441 CC   | :OTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500<br>   |
| Qy<br>Db 1 | 501 G1<br>                | luaspGluCysValGlyGluČjyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520<br>   |
| Qy<br>Db   | 521 Tr<br>  <br> 561 TC   | rpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540<br>   |
| Qy<br>Db   | 541 Va<br>  <br> 1621 GT  | alGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgH1sCys 560<br>   |
| Qy Db      | 561 Le<br>  <br> 1681 TT  | euprocysHisProGlucysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580<br>   |
| Οy         | 581 A1                    | laAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600<br>   |

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 The invention relates to inhibiting expression of a target gene in a cell
by introducing at least two oligoribonuclectides (dsRNAI and II), both
comparison that least part of one strand (s1, S2) of the ds structures in each
comparison of dsRNAI and II are complementary to regions in the target gene. The
method uses antisense inhibition of gene expression using double stranded
comparison (RNAI). The method is particularly used to treat tumours
comparison is especially by Plasmodium or viruses/viroids (pathogenic on
humans, animals or plants). The method provides more effective inhibition
comparison than known methods using a single dsRNA, even at very low
concentrations. When dsRNA has at least one unpaired nucleotide at the
concentrations when dsRNA has at least one unpaired nucleotide at the
concentrations when dsRNA has at least concentration in the cell) is
comproved and efficiency can be increased further by pretreating the cells
with interferon. The present sequence is that of a target DNA of the
 ù
 1860
 1920
620
 640
 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 tumors
 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys
 for treating
that are
 other
 1921 GCTGCCCCGCCGAGCAGAGCCAGCCCTCTGACGTCC 1959
 e.g.
RNAS
 0
 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 Τ;
 Inhibiting expression of target genes, useful by introducing into cells two double-stranded complementary to the target
 C; 1121 G; 719
 Hadwiger P;
 S
 Claim 13; Page 38-39; 100pp; German.
 A
 BP
 ŝ
 SEO
 758 A; 1170
 ABZ35744 standard; DNA; 3768
 Rost
 2001DE-1000588
 2001DE-1000588
 polynucleotide
 entry)
 Limmer S,
 (RIBO-) RIBOPHARMA AG
 (first
 2002-683450/74.
 BP;
 DE10100588-A1
 Sequence 3768
 09-JAN-2001;
 09-JAN-2001;
 07-FEB-2003
 Human ERBB2
 Kreutzer R,
 Alignment Scores:
 18-JUL-2002
1741
 601
 ABZ35744;
 621
 641
 Ношо
 RESULT
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3768 653 0

Length: Matches: Conservative:

1.51e-229 3628.00 100.00%

Percent Similarity:

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120
 180
 240
 100
 300
 120
 360
 140
 420
 160
 480
 180
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 220
 999
 240
 720
 260
 780
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 900
 320
 340
 960
 20
 9
 40
 9
 80
 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu
 GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGCTCCCTGCCAGTCCCGAG
 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla
 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValGlnGlyAsnLeu
 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal
 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln
 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
000
Mismatches:
 Indels:
 Gaps:
 (1-653) x ABZ35744 (1-3768)
100.00%
100.00%
Best Local Similarity:
 121
 101
 61
 201
 21
 41
 61
 181
 81
 161
 181
 221
 661
 781
 841
 961
 501
 261
 281
 301
 901
 321
 Query Match:
DB:
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23
 Kreutzer
 61
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 181
Нишап
 Score:
 SE03
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 1080
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 1681 TTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 1740
 1260
 400
 540
 380
 420
 460
 480
 500
 520
 260
 580
 900
 640
 CCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA
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 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer
 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu
 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
 TGGGGTCCAGGGCCCACTCTGAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC
 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys
 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 (first entry)
 23-JAN-2003
 1141
 1561
 341
 361
 381
 441
 461
 1381
 481
 1441
 501
 1501
 521
 601
 621
 641
 1921
 561
 ABX09987
 ABX09987
 ABX09987
 RESULT
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This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (daRNAI) that has a double stranded that setzended (daRNAI) that has a double stranded to the target gene and the calls are treated with interferon before introduction of daRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) to protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic organisms, animals or plants). Treating the cells with interferon greatly increases the extent to which daRNA can inhibit interferon greatly increases the interferon greatly increases the extent to which daRNA can inhibit are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention.
 180
 240
 100
 09
 80
 9
 interferon; oncogene; cytokine; Id; developmental;
 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGInAspIleGlnGluVa1
 ρλ
 Inhibiting expression of target genes, e.g. oncogenes, in cells, k introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
 3768
653
0
0
0
0
 Conservative:
Mismatches:
Indels:
 Ρ,
 Matches:
 Hadwiger
 Length:
 Disclosure; Page 43-44; 98pp; German.
22
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ERBB2 DNA fragment SEQ ID
 1.51e-229
3628.00
100.00%
100.00%
 Rost
 Oligoribonucleotide; interfer prion; inhibition; human; ds.
 09-JAN-2001; 2001DE-1000587
 09-JAN-2001; 2001DE-1000587
 (1-3768)
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 WPI; 2002-742209/81
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 (1-653) x ABX09987
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Best Local Similarity:
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 Homo sapiens
 Alignment Scores:
Pred. No.:
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 21-NOV-2002
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 sapiens
 13-DEC-2002
 Human HER-2
 21-MAR-2002
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 1441
 1681
 1561
 1621
 1741
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 1861
 1921
 461
 501
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 AAD43935
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 AAD43935
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 RESULT 9
AAD43935
ID AAD4
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 460
 CAGGGCTACGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGG
 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln
 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCTCGTCGTCCCCCTGCACCAA
 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu
 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
 1021
 1081
 1141
 1261
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 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
 GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys
LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu
 tumour;
 Transgenic animal; transgenic; mammary gland cell; HER2; cancer; therapy; apoptosis; cytostatic; human; gene; ss.
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 protein"
 "Human HER2
 Location/Qualifiers
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 CDNA; 3768
 16-MAR-2001; 2001US-0811115
 2000US-189844P
 entry)
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 (first
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 standard;
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 (ERIC/) ERICKSON
(KING/) KING K.
(SCHW/) SCHWALL R
 CDNA.
 US2002035736-A1
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100
 180
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 uces in
protein
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 The invention relates to a transgenic non-human mammal that produces in its mammary gland cells detectable levels of a native human HER2 protein or its fragment. The transgenic animals are useful as tumour models for testing HER2-directed cancer therapies, and for identifying anticancer agents. The animals may also be used as source of cells which can be immortalised in culture, in screening for compounds that have potential as prophylactic or therapeutic treatments of diseases or disorders involving expression of HER2. The anti-cancer molecules are useful for inducing apoptosis or cell death of cancer cells. The present sequence is human HER-2 cDNA.
 New transgenic non-human mammal that produces detectable levels of a native human HER2 protein in its mammary gland cells, useful as tumor models for testing HER2-directed cancer therapies, and for identifying anticancer agents
 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu
 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal
 GACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAGGAGGCTGCGGGAGCTG
 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla
 LeuThrLeuIleAspThrAsnArgSerArgAlaCysH1sProCysSerProMetCysLys
 0 other;
 3768
653
0
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Ë
 G; 719
 C; 1121
 English
 BP; 758 A; 1170
 Schwall
 83pp;
 1.51e-229
3628.00
100.00%
100.00%
 (1-3768)
 Page 24-26;
χ,
 WPI; 2002-401155/43
P-PSDB; AAE26349.
 SEQ3 (1-653) x AAD43935
 King
 Best Local Similarity:
 3768
 Percent Similarity
 Ś
 Alignment Scores:
Pred. No.:
 Example 2;
 21
 41
 301
 361
 Erickson
 Sequence
 61
 61
 181
 101
 121
 141
 421
 161
 181
 481
 Query Match:
DB:
 QQ
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1020 1080 1140 1200 1260 1380 1440 1500 1560 720 320 960 340 360 400 420 440 460 220 099 260 780 280 840 300 900 480 500 520 540 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro CTCACACAGGATAGACACCACCACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAATGGCGCC CCCTGGGACCAGCTCTTTCGGAACCGCACCAAGCTCTGCTCCCACCACCCCAACCGCCCA ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 341 1141 1201 1381 601 661 781 901 1081 1261 481 721 281 841 301 321 196 1021 361 381 461 1441 1561 1621 201 261 401 421 501 1501 521 541 ò g οŽ QQ δ g ò ď ò Q δy qq Qγ qq ŏ g ò Dp Qγ qq δ Q Ω q οy QQ οy qq οy qq ò qq ò g a òγ

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241
 41
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 601
 221
 Query Match:
DB:
 qq
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 1800
 1860
 900
 620
 640
 cell epitope; chitosan; CTL response; cancer; Her2 antigen; cytostatic;
 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu
 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys
 ition relates to a method for inducing or enhancing an immune against a polypeptide antigen in an animal, including human.
 the
 Inducing or enhancing an immune response against an antigen, particularly cytotoxic T-lymphocyte responses, for treating or ameliorating prostate or breast cancer, comprises administering
 1921 GGCTGCCCGCCGCCGAGAGAGCCAGCCTCTGACGTCC 1959
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 653
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 Her2
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2./*tag= a
7/product= "Human Her2
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7/*tag= b
7/0..2250
/*tag= c
 Claim 28; Page 85-90; 97pp; English
 ŝ
 Human; immune response; T-helper
vaccine; prostate cancer; breast
immunostimulant; gene; ds.
 antigen formulated with chitosan
 Mouritsen
 ВР
 AAD43986 standard; DNA; 3768
 27-OCT-2000; 2000DK-0001606.
03-NOV-2000; 2000US-245166P.
18-JUN-2001; 2001DK-0000936.
 26-OCT-2001; 2001WO-DK00705.
 (first entry)
 antigen DNA
 Beier AM, Gautam A,
 2002-463339/49.
 (PHAR-) PHARMEXA AS
 P-PSDB; AAE26366.
 WO200234287-A2
 invention
 Homo sapiens
 13-DEC-2002
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 mat_peptide
 Human Her2
 1681
 581
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 AAD43986;
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The method comprises administering the polypeptide antigen or at least one variant which includes at least one first T-helper cell epitope that is foreign to the animal (foreign TH epitope) and is formulated with chitosan. The polypeptide antigen is weakly immunogenic or non-immunogenic. The invention is used as vaccine. The chitosan and polypeptide antigen or its variant are useful in the preparation of an immunogenic composition for inducing or enhancing an immune response, particularly CTL response, against the polypeptide or protein antigen. The method for inducing or enhancing an immune response is useful in treating or ameliorating cancer, e.g. prostate or breast cancer. The present sequence is human Her2 antigen DNA.
 120
 180
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 220
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 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis
 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspilleGlnGluVal
 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla
 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys
 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu
 T; 0 other;
 3768
653
0
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 C; 1121 G; 719
 BP; 758 A; 1170
 1.51e-229
3628.00
100.00%
100.00%
100.00%
 (1-3768)
 SEQ3 (1-653) x AAD43986
 Score:
Percent Similarity:
Best Local Similarity:
 Sequence 3768
 Alignment Scores:
Pred. No.:
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cytostatic;

```
1801 CCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGAG 1860
 The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least part of one strand has an overhang of 1-4 nuclectides. The method is used to inhibit the has an overhang of 1-4 nuclectides. The method is used to inhibit the humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
 Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to target and having an overhang
 oncogene;
 0 other;
 3768
653
0
0
0
 653
 expression inhibitor;
 GCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCC
 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 .;
H
 G; 719
 ď
 Hadwiger
 German.
 Ç; 1121
 gene expr
gene; ds.
 the invention.
 BP
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 Claim 10; Page 142-143; 203pp;
 758 A; 1170
 1.51e-229
3628.00
100.00%
100.00%
100.00%
 2001DE-100586.
2001DE-1055280.
2001DE-1058411.
2001DE-1060151.
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 3768
 ID NO 52
 2002WO-EP00152
 (1-3768)
 entry)
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 virucide; protozoacide;
 dsRNA1;
 ŝ
 (RIBO-) RIBOPHARMA AG
 SEO
 (first
 WPI; 2002-590671/63
 standard;
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 Ç
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 Percent Similarity:
Best Local Similarity:
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 related
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 26-OCT-2001;
29-NOV-2001;
07-DEC-2001;
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 09-JAN-2002;
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 15-NOV-2002
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 18-JUL-2002
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 1861
 1921
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 641
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 ABV78168;
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 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
 GAGGTGACAGCAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA
 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu
 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnBroGluGlnLeuGlnValPhe
 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro
 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla
 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
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|                                                                    | 381 PheAs<br>                                                          | 401 GluTP<br>                                                                                        | 421 ASPLE<br>     <br> 161 GACC                                | 441 TyrSe<br>      <br> 1321 TACTC                                 | 461 LeuG]<br>      <br> 1381 CTGGC                           |          | 501 GluAE<br>      <br> 1501 GAGG                                        | 521 TrpG]<br>                                                  | 541 ValG]<br>      <br> 1621 GTGG                                                                                                                                           | 561 LeuPi<br>       <br>  1681 TTGCC                         | 581 AlaAs<br>       <br>  1741 GCTGA | 601 ProSe<br>           <br>  1801 CCCAG                     |                                                                 | 641 GlyCy<br>         <br>1921 GGCTG                                     | 12<br>13<br>AD3274                                             | 2743;<br>UL-200                                                          | Human Her-2/ne<br>Human; Her-2/h<br>human leukocyt                       | Homo sapiens.                                                        |
|--------------------------------------------------------------------|------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------------|----------|--------------------------------------------------------------------------|----------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|
| qa                                                                 | δ da                                                                   | Qy<br>Db                                                                                             | Qy                                                             | Qy                                                                 | Oy                                                           | Qy       | δ <sub>ο</sub>                                                           | Oy .                                                           | Qy                                                                                                                                                                          | Qy                                                           | Qy                                   | Qy                                                           | da<br>da                                                        | yo da                                                                    | RESULT<br>AAD3274<br>ID AA                                     | X X X X X X X X X X X X X X X X X X X                                    | XX                                   | so<br>—                                                              |
| 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla 20<br> | 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40<br> | 1 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60   11   11   11   11   11   11   11 | GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 8 | 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuarg 10 | IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly | 1 4      | 141 GInLeuargSerLeuThrGluileLeuLySGlyGlyValLeuIleGlnArgAsnProGln 160<br> | LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 1 | 01 CICIOSIACCAGONCACCATILICIGGANGGACAICIICCACAGONACAGCAGCIGGCI 34 B1 LeuThrLeuIleAspThrAsnArgSerAxgAlaCysHisProCysSerProMetCysLys 20 LIHIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys | 2 7                                  | lycysThrGlyProLysHisSerAspCysLeuAlacysLeuHisPheAsnHis 26<br> | SerGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 28 | 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300<br> | 1 TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisAsnGln | 321 GluValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340<br> | 341 ValcysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360<br> | 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380 |
| Qy                                                                 | Oy<br>Db                                                               | Qy                                                                                                   | 3 6 A                                                          | oy do                                                              | Qy                                                           | Oy<br>Op | Oy<br>Dp                                                                 | oy<br>do                                                       | 0                                                                                                                                                                           | QY<br>QD                                                     | Qy                                   | Qy                                                           | Qy                                                              | Qy                                                                       | Qy<br>Dp                                                       | Qy<br>Db                                                                 | Qy<br>Db                                                                 | QY                                                                   |

resegrecaseseccasesarsreacrecasecastrecressessesses 1620 Her-2/Neu protein; immune response; gene therapy; breast cancer; eukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ds GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys ВР DNA; 3768 DNA. (first entry) er-2/neu protein standard; 

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200 900 220 99

120 360

300

100

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GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu
 GlySerArgCySTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis
 ValCýsTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn
 GTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGTGCCAAT
 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro
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 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions of cancer. The compositions of cancer is and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/New polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating an T cell response in a patient. The invention is useful for stimulating a T cell response in a calculatively form duplex molecules with complementary stretches of the entire Her-2/New gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a colypeptide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu
 GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGCTCCCTGCCAGTCCCGAG 120
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 AlaSerThrGlnValCySThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla
 Kalos MD;
 Her-2/New polypeptide composition useful for t diagnosis of cancer, preferably breast cancer
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
653
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 Lodes MJ,
 "Human Her-2/neu protein"
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 present sequence is human Her-2/neu protein DNA.
 2026..3765
/*tag= b
/note= "Intracellular domain"
 Foy TM,
 9; Page 109-114; 129pp; English
 Location/Qualifiers
1..3768
/*tag= a
 Cheever MA,
 1.51e-229
3628.00
100.00%
100.00%
 2000US-225152P.
2000US-236428P.
2001US-270520P.
 /product= ")
 14-AUG-2001; 2001WO-US41733
 (1-.3768)
 Hand-zimmermann S, Chee
Mcneill PD, Vedvick TS;
 WPI; 2002-280758/32.
P-PSDB; AAE20479.
 (CORI-) CORIXA CORP.
 (1-653) x AAD32743
 Percent Similarity:
Best Local Similarity:
Query Match:
 isolated
 prevention and
 14-AUG-2000;
28-SEP-2000;
 21-FEB-2001;
 misc_feature
 Alignment Scores:
Pred. No.:
 21-FEB-2002
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 Novel
 Claim
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 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; human; gene therapy; gene; ss.
 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
 /product= "Her-2/neu"
 Location/Qualifiers
1..3768
/*tag= a
 BP
 ABA92250 standard; cDNA; 3768
 (first entry)
 Human Her-2/neu cDNA.
 WO200212341-A2
 Homo sapiens
 17-JUN-2002
 14-FEB-2002
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 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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 The present sequence is that of human Her-2/neu oncogene cDNA.

The cDNA encodes Her-2/neu (p185), an oncogenic self protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoporteins.

Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins of the tusion proteins or nucleic acid molecules. In preferred fusion proteins or nucleic acid molecules. In proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein in the form of a vaccine, or by cresponse to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells contained the transfected cells of the animal. The fusion protein, and delivering the transfected cancer, especially breast, ovarian, colon, lung or prostate cancer.

The protein is that specifically react with a Her-2/neu cancer, especially that specifically preact with a Her-2/neu.
 eliciting
 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla
 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu
 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
 remove tumour cells from a sample in
 Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 fusion protein can be used to remove tumour cells from a order to inhibit the development of cancer in a patient.
 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
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 Matches:
Conservative:
Mismatches:
 Indels:
Gaps:
 (CORI-) CORIXA CORP. (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 Disclosure, Fig 15; 141pp; English.
 1.51e-229
3628.00
100.00%
100.00%
03-AUG-2001; 2001WO-US24283
 2000US-0632507
 (1-653) x ABA92250 (1-3768)
 Cheever MA, Gheysen D;
 phosphorylation domain
 WPI; 2002-241743/29.
P-PSDB; AAM51143.
 Percent Similarity:
Best Local Similarity:
 Sequence 3768
 03-AUG-2000;
 Alignment Scores:
 21
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 181
 Query Match:
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 CML;
 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
 CLL;
 ; Her-2/neu; gene; ds; cytostatic; haematological malignancy; C
myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
ic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
in's lymphoma; T cell therapy.
 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 Her-2/neu"
 Location/Qualifiers
1..3768
 "Human
 3768
 2000US-0638280
2000US-0675904
 2001WO-US25408
 /*tag= a
/product=
 entry)
 DNA;
 (first
 Her-2/neu DNA
 standard;
 WO200213847-A2
 13-AUG-2001;
 14-AUG-2000;
28-SEP-2000;
 sapiens
 05-JUN-2002
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 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn
 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu
SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu
 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis
 GTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCCAGTTACCAGTGCCAAT
 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys
 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro
 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polynuclectide encoding the polypeptide. Antique presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hoddykin's lymphoma and non-Hodgkin's lymphoma. This sequence represents DNA encoding human Her-2/neu
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 cal malignancy development by administering immunogenic portion of Her-2/neu, polynucleotide le, or antigen presenting cells expressing the
 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal
 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln
 1leValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu
 other;
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 G; 719
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 Hand-zimmermann
 English
 C; 1119
 Disclosure; Page 66-71; 74pp;
 759 A; 1171
 1.51e-229
3628.00
100.00%
100.00%
 (1-3768)
 Inhibiting haematological
 polypeptide comprising immencoding the polypeptide,
 Æ,
CORP.
 2002-280741/32
 Cheever
 (1-653) x ABK10730
 BP;
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAU77114
CORIXA
 Sequence 3768
 Scores:
 polypeptide.
 polypeptide
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 (CORI-)
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 Query Match
DB:
 No.:
 Alignment ?
Pred. No.:
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1020 1140 1080 1200 1260 1320 1380 1440 1560 1500 1620 240 260 540 200 600 220 099 720 780 280 840 300 900 320 960 340 360 380 400 420 440 460 480 500 520 560 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys AlaGlyClyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis SerGlyIleCysGluLeuH1sCysProAlaLeuValThrTyrAsnThrAspThrPheGlu AGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAG TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn PheaspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 1021 541 181 201 221 661 241 781 841 341 601 721 261 281 301 901 321 961 381 1201 421 1261 441 1321 461 1381 481 1441 1501 541 401 501 521 ŏ g Ω Db δy qq δλ g οy q g δ qq δy g Qγ qq δy αq Qγ qq ŏ δ q pp q g δ δ οχ δ g ò a δ g ŏ

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 The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonuclectide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonuclectides for antisense inhibition of gene expression useful carected against genes present in pathogens (e.g. lasmodium or directed against genes present in pathogens (e.g. lasmodium or cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known captures, probably because the unpaired overhang increases captulity and thus intracellular concentration.
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 Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
cytostatic; virucide; protozoacide; antibacterial; ds.
581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu
 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys
 Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
 Hadwiger P;
 Claim 13; Page 41-42; 104pp; German.
 52.
 Rost S,
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 ABL91709 standard; DNA; 3768
 Human polynucleotide SEQ ID
 09-JAN-2001; 2001DE-1000586
 09-JAN-2001; 2001DE-1000586
 (first entry)
 Limmer S,
 (RIBO-) RIBOPHARMA AG
 WPI; 2002-270454/32
 terminal bases
 DE10100586-C1
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 Kreutzer R,
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 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis
 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
 T; 0 other;
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 Conservative:
Mismatches:
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G; 719
 Matches:
 Length:
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3628.00
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 (1-653) x ABL91709 (1-3768)
 BP;
 Percent Similarity:
Best Local Similarity:
Sequence 3768
 Alignment Scores
 81
 301
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 361
 141
 421
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 481
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 Query Match:
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| 320<br>960                                                      | 340<br>1020                                                     | 360<br>1080                                                    | 380<br>1140                                                    | 400                                                            | 420                                                              | 440<br>1320                                                      | 460<br>1380                                                     | 480<br>1440                                                     | 500<br>1500                                                    | 520<br>1560                                                    | 540<br>1620                                                    | 560<br>1680                                                   | 580<br>1740                                                    | 600<br>1800                                                      | 620<br>1860                                                    | 640<br>1920                                                    |                                               |
|-----------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------|------------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|-----------------------------------------------|
| yrasntyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln<br> | luValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg<br> | 1CysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn<br> | eGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer<br> | eAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe<br> | GluthrLeuglugluilethrGlytyrLeutyrileSeralatrpProAspSerLeuPro<br> | AspleuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla<br> | YrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu<br> | euGlySerGlyLeuAlaLeuIleHiSHiSASnThrHiSLeuCySPheValHiSThrVal<br> | OTTPASPG1nLeuPheArgAsnProHisG1nAlaLeuLeuHisThrAlaAsnArgPro<br> | uAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys<br> | PG1yProG1yProThrG1nCysValAsnCysSerG1nPheLeuArgG1yG1nG1uCys<br> | GluGluCysArgYalLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHiSCys<br> | uProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu<br> | AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys<br> | oSerGlyvalLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu<br> | yAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys<br> | yCysProAlaGluGlnArgAlaSerProLeuThrSer 653<br> |
| 301 T                                                           | 321 G<br> <br>961 G                                             | 341 Va.<br>  <br>                                              | 361 Ile<br>  <br> 081 ATC                                      | 381 Phe                                                        | 401 G                                                            | 421 As<br> <br>                                                  | 441 T)<br> <br> 321 T                                           | 461 L<br>1<br>381 C                                             | 481 Pr<br>                                                     | 501 Glu                                                        | 521 Tr<br>  <br>561 TG                                         | 541 Va<br>  <br>621 GT                                        | 561 Le                                                         | 581<br>741                                                       | 601 Pros<br>       <br>  801 CCC                               | 621 G1:<br>   <br>  861 GG                                     | 641 Gly<br>  <br>  921 GGG                    |
| oy<br>da                                                        | Oy<br>Db                                                        | Qy<br>Db 1                                                     | Qy<br>Ob 1                                                     | Oy<br>Db                                                       | Qy<br>Db 1                                                       | Qy<br>Db 1                                                       | Oy<br>Db 1                                                      | Qy<br>Db 1                                                      | Oy<br>Db 1                                                     | 2y<br>Db                                                       | Qy<br>Db 1                                                     | Qy<br>Db 1                                                    | Oy<br>Db 1                                                     | Qy<br>Db 1                                                       | Qy<br>Db 1                                                     | Qy<br>Db 1                                                     | Qy<br>Db 1                                    |

Search completed: October 15, 2003, 23:49:41 Job time : 669.221 secs

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AC040933 H
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 RESULT 1
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"MODEL=frame+_p7n.model -DEV=xlp

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-OUTFWT=ptc -NORM=ext -HERESTE=500 -MINLENC -MAXLEN-2000000000

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 2888711 seqs, 20454813386 residues
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| 221      | 671                                                                                             | 241     | 731    | 261                             | 791       | 281     | 851  | 301                                | 911          | 321                                 | 971                                    | 341                        | 1031                        | 361                                                               | 1091                                   | 381                                                             | 1151                                                          | 401                                                             | 1211                                                       | 421 | 1271   | 44]                                                                 | 1331 | 461 | 1391 | 481                                                           | 1451                                                       | 501                                                            | 1511 | 521 | 157 | 541                                                             | 1631                                                  | 561 | 1691 | 583                                               |
|----------|-------------------------------------------------------------------------------------------------|---------|--------|---------------------------------|-----------|---------|------|------------------------------------|--------------|-------------------------------------|----------------------------------------|----------------------------|-----------------------------|-------------------------------------------------------------------|----------------------------------------|-----------------------------------------------------------------|---------------------------------------------------------------|-----------------------------------------------------------------|------------------------------------------------------------|-----|--------|---------------------------------------------------------------------|------|-----|------|---------------------------------------------------------------|------------------------------------------------------------|----------------------------------------------------------------|------|-----|-----|-----------------------------------------------------------------|-------------------------------------------------------|-----|------|---------------------------------------------------|
| Qy       | QQ                                                                                              | Qy      | QQ     | Qy                              | qq        | Οy      | QΩ   | QY                                 | qa           | Qy                                  | QQ                                     | δy                         | qq                          | Οy                                                                | QQ                                     | ٥y                                                              | đ                                                             | Qy                                                              | QQ                                                         | οy  | QQ     | Οy                                                                  | Οp   | δy  | QQ   | QY                                                            | QQ                                                         | Qy                                                             | qq   | ΟŸ  | qq  | Qy                                                              | Dp                                                    | Qy  | QD   | AC                                                |
|          | LOCUS AR082744 2385 bp DNA linear PAT 01-SEP-2000 28EINITION Sequence 3 from patent US 5976546. |         | Ž      |                                 | Laus, R., | AL<br>c | urce | BASE COUNT 488 a 780 c 677 g 440 t | nent goorse. | : 1.7e-226 Length: 3628.00 Matches: | it Similarity: 100.00% Conservative: 0 | 100.00% Indels:<br>6 Gaps: | (1-653) x AR082744 (1-2385) | 1 MetGlijenalaalalenCvsardTrnGlv[enjenalajenjennomproproglvala 20 | ### ################################## | AlaSerThrGlnValCvsThrGlvThrAanMatIvsTonlarnIonDroals GarbroClin | GGGAGCACCCAAGTGTGCACCGGCACAGGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG | ThrHis LenAsoMet LenArdHis LenTvrGlnGlvCvsGlnValValGlnGlvAsnIen | ACCACCTGGACATGCTCCGCCACCTCTACCAGGCTGCCAGGTGGTGCAGGGGAACCTG |     |        | 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArqGlnValProLeuGlnArqLeuArq 100 |      |     |      | AsnProfenAsnAsnArhrPhrDroValThrGlvalaSerbroGlvGlvLenardClufen | GACCCGCTGAACAATACCACCCCTGTCACAGGGCCTCCCCAGGAGGCCTGCGGAGGTC | Gln[en]ArgSer[en]thrGln1]e[en]wsGlvGlvVal[en1]eGlnArgsenDroGln |      | [   |     | CICLOCINCONGENCTOCONIIII GIGGENAGONCHICII CCACANGANCANCCIGGCI O | 101 Lettiillettiillillillillillillillillillillillilli |     |      | 0001000100100100000011010400411010404001104000000 |
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AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 7.1 1 Š

| Intelning   Inte | 11 GGCTCCCGCTGCGGGAGAGGTTCTGAGGATTGTCAGAGCCTGACGCGCACTGTCTGT | AGCTGCACTGCCCAGGTCACCTACACACACACACACACGTTTGAG 85 rodluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 30                                                                                 | 321 GluValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340 | 361 IleGlnGluPheAlaGlyCysLysLysLlePheGlySerLeuAlaPheLeuProGluSer 380                                           | 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420 | 441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460 [ |
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| o d o d o o                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                        | do oy                                                                                                                                                                               | 60 G G                                                               | , da 6, da                                                                                                     | 0                                                                    | 60 00 00 00 00 00 00 00 00 00 00 00 00 0                               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 2385<br>S 608                                                | Laus, R., Ruegg, C. Landon. and Wu, H. Immunostimulatory method Patent: US 6080409-A 3 27-JUN-2000; Location/Qualifiers 1. 2385 /organism="unknown" 488 a 780 c 677 g 440 t Scores: | 440 8                                                                | 1 MetGluLeun<br>  H        <br>  11 ATGGGGCGC<br>  21 AlaSerThrG<br>                         <br>  71 GGGGGCCC | ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60      |                                                                        |

| 61 ULEUTHTTYTEUPTOTHTASNALaSerLeuSerPheLeuGlnAspIleGlnGluVal 80                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 431 CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGTCTTGAFCCAGGGGAACCCCCAG 490 161 LeuCysTyrGlnAspThr11eLeuTrpLysAsp11ePheHisLysAshAsnGlnLeuAla 180 161 LeuCysTyrGlnAspThr11eLeuTrpLysAsp11ePheHisLysAshAsnGlnLeuAla 180 161 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1 | 24<br>73<br>79<br>79<br>85<br>85<br>85                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                         | 1031 GTGTGCTATGGCATGGGAGGGGGGGGGGGGGGGGGGGGG                                |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Qy         601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620           Db                                                                                                                                                             | RESULT 3 AR143949 LOCUS LOCUS LOCUS AR143949 LOCUS AR143949 LOCUS DETINITION Sequence 3 from patent US 6210662. DETINITION Sequence 3 from patent US 6210662. AR143949 VERSION KEYWORDS UNKNOWN. ONGANISM UNKNOWN. ONGANISM UNKNOWN. AUTHORS LAUS, R., Ruegg, C. Landon and Wu, H. TITLE Immunostimulatory composition JUNINAL PATENTE TREET PATENTS AUTHORS JUNINAL DETINITION JUNINAL JUNIN | rce<br>NT<br>t Sc<br>::<br>Simi<br>al S | 23 (1-653) x AR143949 (1-2385)  1 MetGluLeuAlaAlauCysArgTrpGlyLeuLeuLeuA  1 |

| 6 Gaps: 0  x AR034479 (1-3768)  MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 2 | 21 ACCCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGCAGGGAAACCTG 61 GluLeuthrTyrLeuProThrAsnalaSerLeuSerPheLeuGlnAspIleGlnGluVal           | 21 Asprocedusoraccaeciciiionasacaeciciiscocciciiciicaecaeciciicaecaecaecaecaecaecaecaecaecaecaecaecaec | 16   LeucysyyclahaspThrileLeuTrpLysaspILePheHistySashanGalchanta   180 | AlaGlyGlyCysAlaArgCysLysGlyProLeuproThrAspCySCysHlsGluGlnCys                                                                                                                                          | 261 SECT97116-C561LucuettisCysProAlaLeuValThrTyAssnffhrsApfhrsPhocolu 280                                                                                                                                                                                                              | on incarcinceinceinceinceinceinceinceinceinceinc                                                                                                             |
|------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|
| DB:<br>SEQ3<br>OY<br>Db                                                                        | 90 00 00 00 00 00 00 00 00 00 00 00 00 0                                                                                               | ra ko a ko a ko                                                                                        |                                                                        | 3 6 6 6 6                                                                                                                                                                                             | d d d d d d                                                                                                                                                                                                                                                                            | oy og                                                                                                                                                        |
|                                                                                                | Oy         501 GluaspGluCysValGlyGluGlyLeuAlaCysHisGInLeuCysAlaArgGlyHisCys         520           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Oy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580                                | 1811   CCCAGGGGTGTGAAACTCTCTCTCTGGTGTTTTTTTTTT                         | RESULT 4  AR034479  LOCUS  AR034479  AR034479  DEFINITION Sequence 1 from patent US 5869445.  ACCESSION AR034479  ACCESSION AR034479.1 GI:5950084  KEYWORDS  SOURCE  Unknown.  ORGANISM  Unclassified | REFERENCE 1 (bases 1 to 3768) AUTHORS Cheever,M.A. and Disis,M.L. AUTHORS Cheever,M.A. and Disis,M.L. TITLE Methods for eliciting or enhancing reactivity to HER-2/neu protein JOURNAL Patent: US 5869445-A 1 09-FEB-1999; FEATURES 1.3768 BASE COUNT 759 a 1171 c 1119 g 719 t ORIGIN | Alignment Scores:  2.84e-226 Length: 3768  Score: Score: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 100.00% Indels: 0 |

| REFERENCE 1 AUTHORS Elickson, S. and Schwall, R. TITLE Methods of treatment using anti-erbb antibody-maytansinoid conjugates JOURNAL Patent: WO 0100244-A 2 04-JAN-2001; FEATURES 1.3768 / Organism="Homo sapiens" / Mol_type="genomic DNA"   // Ab_xref="taxon:9606"   // Ab_xref="ta | Alignment Scores: 2.84e-226 Length: 3768 Pred. No.: 3628.00 Matches: 653 Score: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 6 Gaps: 0 | SEQ3 (1-653) x AX060704 (1-3768)   Ox                                   |  | 101 IlevalargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 101 IlevalargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 101 Illilililililililililililililililililil                                                                     |                                                                                                                                                                                                                                                                                                                                                 | Qy         201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys         220           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII                                                                                                                                          |
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| 241 ALBALIGUI POPRITHE IL PROUVBRILSSEN MENOS PREMANDE AND        |                                                                                                                                                                             | RESULT 6         AX201817       3768 bp       DNA       linear       PAT 30-AUG-2001         LOCUS       AX201817       ACCESION       AX201817         ACCESSION       AX201817       GI:15391666         KEYWORDS       Homo sapiens (human) | ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE AUTHORS Cheever, M.A. and Hand-Zimmermann, S. TITLE Compounds and methods for prevention and treatment of her-2/ neu associated mallgnancies JOURNAL Patent: WO 0153463-A 1 26-JUL-2001; | CORIXA CORPORATION (US) FEATURES Location/Qualiflers 1. 3768   Applied to the control of the con | /mor_tref="taxon:9606"  CDS 1. 3768                              | /codousstarto-<br>/protein_id="CAC60126.1"<br>/db_xref="G1:15391667"<br>/translation="MELAALCRALLALLPPGAASTQVCTGTDMKLRLPASPETHLD<br>M.BHIYOGCOVYOGNIFT WILDMASSIGETONIORUSYTIAHMOVEDIORIPHY | REACHER SOUT THE ALL STREET THE STREET STREE | SKPCARVCYGLGMEHLARDON THE THILDS DESCRIPTOR THE THE STATE STATE THE STATE TH | LACAGUAGA MARANG PERPUCANAN MARANG MA | POGENY LEVBEN SERVICE OF THE STANDELLIDES I WARD VESET VS TALLOLICLE SI VOLVI<br>OLMPYGCLLDHVRENKGERLEGODLLINGCMOLAKGMSYLEDVRLVHRDLAARNVLVKSP<br>NHVK I TDFGLARLLDI DETEYHADGGRVD I KWMALES I LRRRFTHQSDVWSYGVTVWE<br>LMTFGRARYDGGI PARET PDLLERGERLEPOPLICT DVYM INVKKWHI DSECKER PREFEEL<br>VGESSEMA PDROBENVI TOMORY CARA GODI GETTANDEN VIDA REVI V DOGGE | YSEZSMANDEGEN VY KONEDISANSFILDED ET RINGLIDDUNGLUNGELET FYKUGUE<br>FCPDPAPGAGGWYHHHHRSSSTRSGGGDLTLGLEPSEEBAPRSPLAPSEGAGSDVPDG<br>DLGMGAAKGLQSLPTHDPSPLQRY SEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR<br>POPPSPSREGPLPARPAGATLERPRYLLSFORKNGVVKDYPSFGGAVENPFEYLTPQGGAA | 759 a                                                                | 2.84e-226<br>3628.00<br>100.00%                                      | Local Similarity: 100.00% Mismacches: // Match: 6 Gaps:          | 23 (1-553) x AX201817 (1-3768)                                  |
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| 241 AlaAlaGlyCysPhrGlyProLysBitsSerhapCysLeuhlacyBeanHis 721 GCTGCGGCTGCAGGGCCCAAGCACTCGACTGCCTGCCTGC | 9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                     | RESULT AX2018 LOCUS DEFINI ACCESS VERSIO KEYWOR                                                                                                                                                                                                | OF REFE AU                                                                                                                                                                                                                                                                                                                                             | FEAT                                                                                                                                   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Alignm<br>Pred.<br>Score:<br>Percen                                  | Best<br>Quer<br>DB:                                              | SEO33                                                           |
|                                                                                                       | 41 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheasnHis 21 GGTGCGGCGCGCCCCCCCAGCCTCTGCTGCTGCTGCTGCTGCTCCCCCCACTTCAACCAC 52 GGTGCGGCGCGCCCCAAGCACTCTGACTGCTGCCTGCCTG | 01 TyrasnfyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln                                                                                                                                                                                | ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn                                                                                                                                                                                                                                                                                           | 81 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GluthrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro<br> | AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla<br>                                                                                                                            | TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 61 LeuGlySerGlyLeuAlaLeuIleH18H1SASnThrH18LeuCySPheValH18ThrVal<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 81 ProftpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 01 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys<br>                                                                                                                                                                                                                                                                                           | 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys<br>                                                                                                                                                                                           | 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys<br> | 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu<br> | 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys | 01 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu |

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 7026. 3765

7026. 3765

2968. 3176

7026="phosphorylation domain (PD) of human Her-2/neu"

2968. 3144

7026="preferred portion of the phosphorylation domain

(delta PD) of human Her-2/neu"
 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
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 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla
 'note="extracellular domain (ECD) of human Her-2/neu"
 BEECHAM BIOLOGICALS S.A.
 POPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV"
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 protein"
Patent: WO 0212341-A 3 14 ELL CORIXA CORPORATION (US); SMITHKLINE LOCATION/Qualifiers
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/note="human Her-2/neu pro
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 GlySerArgCySTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
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 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro
 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla
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| BASE                                                       | Aligr<br>Pred<br>Score<br>Perce<br>Best<br>Query<br>DB: | SEQ3                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| 1321 TACTCGCTGACCCTGCAAGGGCTGGGCTGGGCTGGGCCTGCTCACTGAGGGAA | 580<br>1740<br>600<br>1800                              | 601 ProSerGlyVallysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620 | AX384604 3768 bp DNA linear PAT 19-MAR-2002 Sequence 1 from Patent W00214503.  AX384604 1 GI:19577806  AX384604.1 GI:19577806  AX384604.1 GI:19577806  Homo sapiens (human)  ISM Homo sapiens (human)  Homo sapiens (human)  Location, S., Cheever, M.A., Foy, T.M., Lodes, M.J., Kalos, M.D., Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  Band-Zimmermann, S., Cheever, M.A., Foy, T.M., Lodes, M.J., Kalos, M.D., Mcneill, P.D. and Vedvick, T.S.  Compositions and methods for the therapy and diagnosis of her-Z/neu-associated maliannies  AL Patent: W0 0214503-A 1 21-FEB-2002;  CORIXA CORPORATION (US)  Location/Qualifiers  Location/Qualifiers  Location_Lype="enomic DNA"  /db_xref="classociated" conduct"  /db_xre |
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LCYOPTILWEDIFHKNNOLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCOSLTRT
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PQPPSPRRGGLDVANYWDQDPPRRGAPPERFRATARGGAAPERGAASDVPUP
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| 961 GAGGTGACAGCAGGATGGAACACAGGGGTGTGAGAAGTGCAGCAAGCCCTGTGCCGA 1020 341 VALCYSTYTGLYLGHOLYMETGLUHISLEUARGGLUVALARGALAVALTHISERALAASN 360                                | 61 IlegingluphealagiyCysLysLysLiePheGiySerLeualapheLeuProGluser 3 | PheAspOlyAspFroAlaSerAssThrAlaProLeuGlnProGlugInLeuGlnValPhe 4        |                                                                       | 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440<br> | 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460<br> | 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480 | 481 ProtrpaspGlnLeuPheargasnProHisGlnalaLeuLeuHisThralaasnArgPro 500 | 501 GluaspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520   11111111111111111111111111111111111 | 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 | 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560<br> | 561 LeuprocysHisProGlucysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 | 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 | 601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620<br> | 621 GlyalaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640<br> | 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653<br> |                                                | AX467229<br>AX467229.1 GI:21900511     |
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| Db<br>Qy<br>Db                                                                                                                                                         | Qy                                                                | Qy<br>Db                                                              | Qy<br>Dp                                                              | Qy<br>Db                                                                 | Qy<br>Db                                                                 | Oy<br>Db                                                             | QY<br>Db                                                             | QY                                                                                                         | QY                                                                   | QY                                                                       | QΥ<br>Db                                                             | QY                                                                   | QY<br>Db                                                                 | QY<br>Db                                                                 | Qy<br>Db                                            | RESULT 10<br>AX467229<br>LOCUS<br>DEFINITION   | ACCESS<br>VERSIC<br>KEYWOI             |
|                                                                                                                                                                        |                                                                   |                                                                       | •                                                                     |                                                                          |                                                                          |                                                                      |                                                                      |                                                                                                            |                                                                      |                                                                          |                                                                      |                                                                      |                                                                          | ,                                                                        |                                                     |                                                |                                        |
| Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 SEQ3 (1-653) x AX465456 (1-3768) | 1 MetGluLeuAlaAlaL<br>                                            | Oy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40 | Oy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60 | uVal<br>                                                                 | ProLeuGlnArgLeuArg 10<br>                                                | JALAVALLEUASPA<br>                                                   | roLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu<br>         | 41 GlnLeuArgSerLeuThrGluIleLeuLysGlyCalLeuIleGlnArgAsnProGln<br>                                           | LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 18<br>  | SLYS 20<br>     <br> TAAG 60                                             | 61ySerArgCysTrpG1yG1uSerSerG1uAspCysG1nSerLeuThrArgThrVa1Cys<br>     | sGluGlnCys                                                           | 11yCysThrG1yProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 2<br>             | SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu             | OGLUGLYARGTYRThrPheGlyAlaSerCysValThrAlaCysPro 30   | ThraspvalGlySerCysThrLeuValCysProLeuHisAsn<br> | nArgCysGluLysCysSerLysProCysAlaArg<br> |

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Beler,A.W., Gautam,A. and Mouritsen,S.R.
Novel therapeutic vaccine formulations
Patent: WO 0234287-A 3 02-MAY-2002;
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Location/Qualifiers
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Homo
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| 6. LendlySarGlyLenAlaLeuTleHisAarnthrHisLouCysPhaValHisThrNa 1881  6. COGGGCACTGGCACTGCCCCACCTACTCCCCCTTTTTTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                          | 90 OX                          | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                           | 90<br>00<br>00                                                                                                                                                                                                                      | \$ 6 \$ 6 \$ 6 \$ 6 \$ 6 \$ 6 \$ 6 \$ 6 \$ 6 \$ 6                                                                                                                                                                                         |                                                                                                                                     |
| 6. TedGlySarGlyLenAlaLeuTleHisHin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                  |                                                                    |                                                                 |                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                           |                                                                                                                                     |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480 | LeuProcysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 58  [ | 1                                                               | AX481438.1 G1:22316352  Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Kreutzer,R., Limmer,S., Rost,S. and Hadwider,P. | Method for inhibiting the expression of a target Patent: WO 02055693-A 52 18-JUL-2002; Ribopharma AG (DE) Location/Qualifiers 1. 3768 //organism="Homo sapiens" //mol_type="genomic DNA" //db_xxef="taxon:9606" 758 a 1170 c 1121 g 719 t | 2.84e-226 Length: 376<br>3628.00 Matches: 653<br>100.00% Conservative: 0<br>100.00% Mismatches: 0<br>100.00% Indels: 0<br>6 Gaps: 0 |

| JOURNAL Patent: US 5968748-A 1 19-OCT-1999;  FEATURES  Location/Qualifiers  Location/Qualifiers  1.4473  BASE COUNT  ORIGIN  Alignment Scores: Pred. No.: 3.45e-226  Percent Similarity: 100.00%  Best Local Similarity: 100.00%  Ouery Match: 6  DB:: 6  SEQ3 (1-653) x AR080259 (1-4473)                                                                                 | 1 MetGluLeuAlaalaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuDroProClyAla | 255 GAACTCACCTACCTACCCACCACTGTCCTTCCTGCAGGATATCCAGGAGGTG 414     Qy                                                                                                                                                                                                                                                                | 655 CTCTGCTACCAGGACTTTTGCGAAGGACTCTTCCCAGGACCACCAGCTGCTTGTGTTTTGCGAAGGACTCTTCCCCAGGACCACCAGCTGCTTTGTGTGTTTGTCGAAGGACTCTTCCCCAGGACCACCAGCTGCTTTTGTTGTTGTTTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Db 955 AGTGGCATCTGTGAGCTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAG 1014                                                          |
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| 20 Gityserkgrygripolygluserserciukspryschniscreuchnisty 20 mp 139 27 Jacoby gryghtheliyoluserserciukspryschniscreuchnisty 24 ms. 24 machyglygripolygluserserciukspryschnisty 24 ms. 25 m | 1915 TYCCCGCCCCCGACTGCTCACCCCACAATGCCTCACTGCACTGCTCACTCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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| 101 GlySerArgCySTEDGlyGluSerSerGluAspCysGlnSerLeuthrArgThrVallcys 111 [111 [111 [111 [111 [111 [111 [111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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gb_htc:*
 JUNC_SEQ8_SEQ5
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 Database
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Simpson, A.J.
 Simpson, A.J.
 Percent Similarity:
Best Local Similarity:
Query Match:
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 BASE COUNT
 MEDLINE
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Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.

78 c 79 g 69 t
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-NF0251-
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Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 EST 12-JAN-2001
mRNA sequence.
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 294 bp mRNA linear CM4-CT0574-101100-428-f11 CT0574 Homo sapiens CDNA, BF757857
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 83.00
88.89%
88.89%
51.88%
 1. .278
 Simpson, A.J.
 Homo sapiens
 Best Local Similarity:
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 Percent Similarity:
 Alignment Scores:
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 Pred. No.:
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 BASE COUNT
 ORGANISM
 MEDLINE
PUBMED
 JOURNAL
 RESULT 2
BF757857
LOCUS
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 AUTHORS
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 FEATURES
 COMMENT
 ORIGIN
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 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM46t2=CM4-CT0574-10100-428*filkt3=2000-11-106t4=1)
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High quality sequence start: 9
High quality sequence start: 9
High quality sequence storp: 294.
 Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 expressed
 Shotgun sequencing of the human transcriptome with ORF
 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 294
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Conservative:
Mismatches:
Indels:
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 Homo sapiens (human)
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88.89%
51.88%
 sequence tags
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into the pUC 18 vector. Reverse transcription of tissue
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 Email: asimpsonebludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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Location/Qualifiers
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Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
EST analysis of human adipose gene expression
 378 bp mRNA linear EST 20-FEB-20 1005398 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens CB266492
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
 Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
 348
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Mismatches:
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Seq primer: GTTGGTACCCGGGAATTC.
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COMMENT
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 REFERENCE
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 FEATURES
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 ŏ
 g
 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Project. This entry can be seen in the following URL
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 Bukaryotza, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 348)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 EST 30-MAR-2000
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 118 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAGCCCTTGGACAGCACCTTC 95
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QV-BT225-050599-038 BT225 Homo sapiens cDNA, mRNA sequence.
AI909847
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 337
16
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Matches:
Conservative:
Mismatches:
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 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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88.89%
51.88%
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SOURCE
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 TITLE
 RESULT
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EST 20-FEB-2003

30

423 116 0 0 0

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Oganger A., Fobo G.,
to an EcoR I adaptor, digested with Not I, and cloned directionally into pTyT3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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 This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKFZp686M12198) is available at the RZPD in Ber
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERWANY
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Mismatches:
 09-MAY-2003 (Rel. 75, Created)
09-MAY-2003 (Rel. 75, Last updated, Version 1)
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 Location/Qualifiers
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 Homo sapiens (human)
 Han M., Wiemann S.;
 Best Local Similarity:
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modified polylinker: Site_l: EcoR I; Site_2: Not I;
UI-E-CKI is a normalized cDNA library containing the
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library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dr primer
containing a Not I site. Double stranded cDNA was ligated
 Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
COne Distribution: Researchers may obtain clones from Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Bonaldo,W.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
 Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9565
Fax: 319 335 9565
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 Contact: Soares, MB
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
Side Frontier Korean EST Project 2001
Unpublished
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Visecong-gu, Daejeon 305-333, South Korea
Fat: +82-42-860-4470
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Mismatches:
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88.89%
51.88%
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Best Local Similarity:
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 BM85442]
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 BASE COUNT
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JOURNAL
COMMENT
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 1 (bases 1 to 496)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 BM795191 496 bp mRNA linear EST 05-MAR-2002
K-EST0076753 S21SNU520 Homo sapiens cDNA clone S21SNU520-26-D05 5',
 converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplDf by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
T=1: +82-42-860-44470
Fax: +82-42-860-4409
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Unpublished
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 TITLE
JOURNAL
COMMENT
 REFERENCE
AUTHORS
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 RESULT 8
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 FEATURES
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PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded CDNAs prepared from original
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 536)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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 liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
 Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea 7tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 5 row: C column: 08 High quality sequence stop: 536.
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Genome Research Center
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intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 6ont. The cDNA vector as
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli ToplOF' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 - 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
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 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseeng-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
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strand cDNA was synthesized from oligo dT-selected mRNA by paining with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The contained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full.length enriched cDNA libraries constructed by this method are 150 c 167 g 114 t
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with tabacco acid pyrophosphatase (TAP). The decaped
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boun dong Yuseong-gu, Daejeon 305-333, South Korea
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 .;
 Homo sapiens mRNA; EST DKFZp686M16257_r1 (from clone DKFZp686M16257)
 B., Amid C., Osanger A., Fobo
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMF2 (Biomedical Research Center at the Heinrich-Heiner-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKF2p680M16257) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum. Hauhmarwar 6
 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERWANY
 e contact the RZPD: Ressourcenzentrum, Heubnerweg 6, Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 574)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
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 Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Feax: +82-42-860-4470
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
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 clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.

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 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERWANY
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CURRENT PEPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR FILING DATE: 2001-08-10

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Publication No. US20020193329A1

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APPLICANT: Cheever, Martin A.
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APPLICANT: Wedvick, Thomas SS.
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FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SSOTUD 0.44
 1755
16
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2
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 Conservative:
Mismatches:
Indels:
 Matches:
Conservative:
Mismatches:
 JUNC_SEQ8_SEQ5 (1-30) x US-09-930-125-4 (1-1767)
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; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
 Sequence 7, Application US/09930125; Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Hand-Zimmerman, Susan, APPLICANT: Cheever, Martin A.
APPLICANT: FOY, Teresa M.
APPLICANT: Lodes, Michael J.
 83.00
88.89%
88.89%
51.88%
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-930-125-6
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 LENGTH: 1755
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 US-09-930-125-4
 US-09-930-125-7
 US-09-930-125-4
 Query Match:
 Sequence 14, Application US/10378393
; Fublication No. US20030182668A1
; Fublication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: BOL, David K.
; APPLICANT: Carboni, Joan M.
APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEO ID NOS: 23
; SOFTURARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 1713
 Sequence 6, Application US/09930125
Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Hand-Zimmerman, Sisan
APPLICANT: Cheever, Martin A.
APPLICANT: Foy, Teresa M.
APPLICANT: Kalos, Michael D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Object Of the APPLICANT: Wedvick, Thomas S.
APPLICANT: OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-Z/NEU-ASSOCIATED MALIGNANCIES
 1713
16
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ8_SEQ5 (1-30) x US-10-102-806-165 (1-1115)
 JUNC_SEQ8_SEQ5 (1-30) x US-10-378-393-14 (1-1713)
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 or
 ; NAME/KEY: misc_feature
; LOCATION: (394)
; CTHER INFORMATION: n equals a,t,g,
US-10-102-806-165
 OTHER INFORMATION: n equals a,t,g,
 0.00225
 0.00141
 83.00
88.89%
88.89%
51.88%
 83.00
88.89%
88.89%
51.88%
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-14
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 RESULT 2
US-10-378-393-14
 US-09-930-125-6
 Pred. No.:
 Score:
 Score:
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junc\_seq8\_seq5.rnpb

Page

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APPLICANT: Wong, Tai W.
APPLICANT: Wong, Tai W.
APPLICANT: Lee, Francis Y.
TITLE OF INVENTION: TRANSENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVAT
TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
FILE REFERENCE: D0254 NP
CURRENT APPLICATION NUMBER: US,10/378,393
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,889
PRIOR PLILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
 APPLICANT: Elizabeth Singer
APPLICANT: Raif Landgraf
APPLICANT: Raif Landgraf
APPLICANT: Raif Landgraf
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
FILE REFERENCE: 30448.103-US-U1
CURRENT APPLICATION NUMBER: 105/10/207,498
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/308,431
PRIOR APPLICATION NUMBER: 60/308,431
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 3765
16
0
2
0
0
 2411
16
0
2
0
0
 Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 JUNC_SEQ8_SEQ5 (1-30) x US-10-378-393-10 (1-2411)
 Length:
Matches:
 Length:
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 JUNC_SEQ8_SEQ5 (1-30) x US-10-207-498-5 (1-3765)
 Indels:
 Sequence 5, Application US/10207498; Publication No. US20030143568A1; GENERAL INFORMATION:
 APPLICANT: Bol, David K.
APPLICANT: Carboni, Joan M.
APPLICANT: Rowley, Ronald B.
 83.00
88.89%
88.89%
51.88%
 83.00
88.89%
88.89%
51.88%
 ORGANISM: Homo sapiens
 TYPE: DNA
ORGANISM: Homo sapiens
 ; LOCATION: (1)...(3765)
US-10-207-498-5
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
Query Match:
 GENERAL INFORMATION:
 NAME/KEY: CDS
 Alignment Scores:
 LENGTH: 2411
TYPE: DNA
 Alignment Scores:
 LENGTH: 3765
 US-10-378-393-10
 US-10-207-498-5
 Query Match:
 Pred. No.:
 RESULT 8
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 Sequence 5, Application US/09930125
Fublication No. US2002019332941
GENERAL INFORMATION:
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Fersa M.
APPLICANT: Foy, Tersa M.
APPLICANT: Kalos, Michael J.
APPLICANT: Moreill, Particia D.
APPLICANT: Moreill, Particia D.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
FILE REFERENCE: 2101121.54
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 201008: 25
SECTION NOWER: FASLESQ for Windows Version 3.0
APPLICANT: Kalos, Michael D.
APPLICANT: MONEIL, Patricia D.
APPLICANT: WONEIL, Patricia D.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1773
 1773
16
0
2
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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 JUNC_SEQ8_SEQ5 (1-30) x US-09-930-125-5 (1-1806)
 ; Sequence 10, Application US/10378393 ; Publication No. US20030182668A1
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 83.00
88.89%
88.89%
51.88%
 0.00238
 83.00
88.89%
88.89%
51.88%
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-930-125-5
 ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Alignment Scores:
 RESULT 7
US-10-378-393-10
 LENGTH: 1806
 US-09-930-125-7
 US-09-930-125-5
 TYPE: DNA
 SEQ ID NO 5
 Query Match:
 Pred. No.:
 Pred. No.:
 Score:
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RESULT

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13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 Sequence 9, Application US/09854356; Patent No. US20020177567A1; GENERAL INFORMATION:
 APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Foy, Teresa M.
APPLICANT: Lodes, Michael J.
APPLICANT: Kalos, Michael D.
APPLICANT: MONEILI, Patricia D.
APPLICANT: Wedvick, Thomas S.
 Sequence 1, Application US/09930125; Publication No. US20020193329A1; GENERAL INFORMATION:
 0.00532
83.00
88.89%
88.89%
51.88%
 ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 RESULT 12
US-09-930-125-1
 TYPE: DNA
 FEATURE:
 Query Match:
 ŏ
 g
 2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCCATGGACATGCACCTTC 3012
 APPLICANT: Erickson, Sharon
APPLICANT: Erickson, Sharon
APPLICANT: Schwall, Ralph
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 2
LENGHH: 3768
 WESOUR

Sequence 8, Application US/09811123

Sequence 8, Application US/09811123

Sequence 8, Application US/09811123

Sequence 8, Application US2002001187A1

SERNET NO. US2002001187A1

APPLICANT: Ralph Schwall

TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB

TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB

TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB

TITLE OF INVENTION: MATEROY ANTIBOY MAYTANSINOID CONJUGATES

CURRENT APPLICATION NUMBER: US/09/811,123

CURRENT FILING DATE: 2000-10-05238,327

PRIOR FILING DATE: 2000-10-05238,327

PRIOR FILING DATE: 2000-10-05238,327

PRIOR FILING DATE: 2000-10-05238

NUMBER OF SEQ ID NOS: 11

SEQ ID NOS

SEQ ID NOS

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Conservative:
Mismatches:
Indels:
Gaps:
 Conservative:
Mismatches:
Indels:
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 Length:
Matches:
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 Gaps:
 ; Sequence 2, Application US/09811115; Patent No. US20020035736A1; GENERAL INFORMATION:
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83.00
88.89%
88.89%
51.88%
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88.89%
88.89%
51.88%
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8
 TYPE: DNA
CORGANISM: HOMO Sapiens
US-09-811-115-2
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Alignment Scores:
 US-09-811-115-2
 Query Match:
 Pred. No.:
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õ g

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NAME/KEY: CDS

LOCATION: (1)..(3768)

OTHER INFORMATION: human HER-2/neu protein

NAME/KEY: misc_feature

LOCATION: (1)..(1959)

OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu

NAME/KEY: misc_feature

LOCATION: (2026)..(3765)

OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu

NAME/KEY: misc_feature

LOCATION: (2968)..(3765)

OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu

NAME/KEY: misc_feature

LOCATION: (2968)..(3144)

OTHER INFORMATION: preferred portion of the phosphorylation domain

OTHER INFORMATION: (delta PD) of human HER-2/neu
2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGTCCCTTGGACGAGCACTTC 3012
 2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTC 3012
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 3768
16
0
2
0
0
 APPLICANT: CHESVEL, FALLLIN...

APPLICANT: Gheysen, Dirk
APPLICANT: Greysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKillen Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2001-01-28
PRIOR PILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VOICE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 9
LENGTH: 3768
 Conservative:
Mismatches:
 JUNC_SEQ8_SEQ5 (1-30) x US-09-854-356-9 (1-3768)
 Length:
Matches:
 Indels:
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APPLICANT: Scholler, Nathalie B.
 Query Match:
 ..
Q
 Pred. No.:
 RESULT 15
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES FILE REFERENCE: 210121.54 P. CURENT APPLICATION NUMBER: US/09/930,125 CURRENT FILING DATE: 2001-08-14 NUMBER OF SED ID NOS: 25 SOFTWARE: FastsEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 2768
 Sequence 1, Application US/10313644

Publication No. US20030157119A1

GENERAL INFORMATION:
APPLICANT: Caiger, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Hand-Zimmerman, Susan
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
CURRENT PRILICAL SUCCESSORY
CURRENT PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: RastSEQ for Windows Version 3.0
LENGTH: 3768
 3768
16
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
 JUNC_SEQ8_SEQ5 (1-30) x US-09-930-125-1 (1-3768)
 JUNC_SEQ8_SEQ5 (1-30) x US-10-313-644-1 (1-3768)
 Indels:
 Sequence 5, Application US/09441411 Publication No. US20030008342A1 GENERAL INFORMATION:
 0.00532
83.00
88.89%
88.89%
51.88%
 0.00532
83.00
88.89%
88.89%
51.88%
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; LOCATION: (1)...(3765)
US-09-930-125-1
 ; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1
 TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
 TYPE: DNA
ORGANISM: Homo sapien
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 US-10-313-644-1
 US-09-441-411-5
 FEATURE:
 Pred. No.:
 RESULT 14
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US-101-510-81

| Sequence 81, Application US/10101510
| Sequence 81, Application US/10101510
| Publication No. US20030148295A1
| GENERAL INFORMATION:
| APPLICANT: WAN, JACKSON
| APPLICANT: WAN, JACKSON
| TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
| FILE REFERENCE: 15117, 0012
| CURRENT APPLICATION NUMBER: US/10/101,510
| PRIOR FILING DATE: 2001-03-20
| PRIOR FILING DATE: 2001-03-20
| NUMBER OF SEQ ID NOS: 805
| SOFTMARE: PATENTIN VET: 2.1
 4473
16
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 4473
16
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2
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APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegrd
APPLICANT: Hellstrom, Karl Erik
TILE OF INVENTION: SURRACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
 Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 JUNC_SEQ8_SEQ5 (1-30) x US-10-101-510-81 (1-4473)
 Length:
Matches:
 JUNC_SEQ8_SEQ5 (1-30) x US-09-441-411-5 (1-4473)
 Matches:
 Indels:
 Gaps:
 Search completed: October 17, 2003, 03:53:14 Job time : 34.0111 secs
 83.00
88.89%
88.89%
51.88%
 83.00
88.89%
88.89%
51.88%
 LENGTH: 4473
TYPE: DNA
CRGANISM: Homo sapiens
US-09-441-411-5
 ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 LENGTH: 4473
 Alignment Scores:
 US-10-101-510-81
 SEQ ID NO 81
 TYPE: DNA
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APPLICANT: Disis, Mary L.

TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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 1, 22,
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Sequence 1,
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Sequence 1
Sequence 1
 Sequence 3
Sequence 3
Sequence 3
 Sequence 4
Sequence 3
Sequence 1
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Sequence
 Sequence
 Seguence
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
US-08-579-823A-3
US-09-34-195-3
US-09-776-251-3
US-09-776-251-10
US-09-5776-251-10
US-09-547-435-25
US-09-547-435-23
US-09-103-840A-2
US-09-103-840A-2
 US-09-328-352-430
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US-09-358-856C-5
US-09-25-388-5
 920010.448C7
 NAME: STARKEY, RICHARD G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
 Sequence 1, Application US/08625101 Patent No. 5869445
 APPLICANT: Cheever, Martin A. APPLICANT: Disis, Mary L.
 ATTORNEY/AGENT INFORMATION:
2385
2385
153
201
201
816
1938
2316
2604
440375
4411529
4411529
1368
2691
2691
536165
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634
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634
634
864
1404
2340
 Washington
 GENERAL INFORMATION:
 98104-7092
 CITY: Seattle
 USA
 COUNTRY:
 US-08-625-101-1
 STATE:
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Sequence 1, Appli
Sequence 1, Appli
 26, Appl
9, Appli
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1, Appli
11, Appli
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US-09-056-105-26
US-08-229-515A-9
US-08-645-865-9
US-09-167-132-4
US-09-877-11
 1 ERGCPAEQRASPVTFQNEDLGPASPLDSTF 30
 Total number of hits satisfying chosen parameters:
 US-08-229-515A-14
US-08-645-865-14
US-09-146-283-3
 569978 seqs, 220691566 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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 Minimum DB seq length: 0
Maximum DB seq length: 20
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51.9
50.6
50.6
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 Database :
 Sequence:
 Searched:
 Run on:
 Result
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 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 APPLICANT: Oppermin, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: BLOSynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
 3768
16
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0
 NAME/KEY: CDS
LOCATION: 1..3768
OTHER INFORMATION: /note= "product = "cerB-b2"
 COMPUTER REALPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
 Length:
Matches:
Conservative:
Mismatches:
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 STREET: Exchange Place, 53 State Street CITY: Boston STATE: Massachusetts
 Indels:
 FILING DATE:
CLASSIECCATION: 424
CLASSIECCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
TELEFAX: (617) 248-7100
TELEFAX: (617) 248-7100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
 US-08-356-786-1; Sequence 1, Application US/08356786; Patent No. 5877305; GENERAL INFORMATION:
 Huston, James S.
 LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 83.00
88.89%
88.89%
51.88%
SEQUENCE CHARACTERISTICS
 TYPE: nucleic acid
STRANDEDNESS: single
 MOLECULE TYPE: CDNA
 Score:
Percent Similarity:
Best Local Similarity:
Query Match:
 linear
 COUNTRY: USA
 Alignment Scores:
 NAME/KEY:
 ; LOCATION:
US-08-625-101-1
 APPLICANT:
APPLICANT:
 FEATURE:
 Pred. No.:
 RESULT 2
 οy
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA STATE: PA COUNTRY: PA ZIP: 19103
 111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 111
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 Sequence 1, Application US/09048804
Patent No. 5968748
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NATA:
APPLICATION WAMBER: US/09/048,804
FILING DATE: Herewith
 Length:
Matches:
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Mismatches:
 Conservative:
Mismatches:
 Length:
Matches:
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 JUNC_SEQ8_SEQ5 (1-30) x US-09-048-804-1 (1-4473)
 Indels:
 Indels:
 ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGIENATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-2913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 LENGTH: 4473 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
 83.00
88.89%
88.89%
51.88%
 83.00
88.89%
88.89%
51.88%
 Percent Similarity:
Best Local Similarity:
 Best Local Similarity:
 CLASSIFICATION:
 Percent Similarity:
 Alignment Scores:
Alignment Scores:
 US-09-056-105-26
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30303
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 JS-08-229-515A-9
 US-08-645-865-9
 US-08-645-865-9
 US-09-167-322-4
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No:
 RESULT
 Sequence 9, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: DEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
COUNTRY: usa
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: WING THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT PILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 4473
 COMPUTER: FLOPPY disk

COMPUTER: IBM PC compatible
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COMPUTER: IBM PC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFRENCE/POCKET NUMBER: 1414.608
TELEPHONINICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEPHONE: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEGUENCE CHRAACTERISTICS:
LENGTH: 4530 base pairs
TTRANDENESS: single
TOPPOLOGY: linear
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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 Gaps:
 83.00
88.89%
88.89%
51.88%
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-056-105-26
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 US-08-229-515A-9
 Query Match:
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Sequence 9, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
APPLICANT: RAZIUDIN
TITLE OF INVENTION: REBE2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: REBE2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CONTY: ALLanta
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTONEY/ACBNT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
REGISTRATION NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEPAX: 404-688-0770
TELEPAXION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Mismatches:
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Mismatches:
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 Indels:
 LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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88.89%
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51.88%
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51.88%
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 Percent Similarity:
Best Local Similarity:
Query Match:
 STATE: Georgia
COUNTRY: usa
 Percent Similarity:
Best Local Similarity:
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junc\_seq8\_seq5.rni

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FEATURE:
 g
 δ
 qq
 ò
 COUNTY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/167,322
FILING DATE: OT-OCT-1998
CLASSIFICATION: <UNKNOWN>
 APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M. England, James M. TITLE OF INVENTION: CANCER VACCINE NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Suite 1800, Two Penn Center Plaza CITY: Philadelphia
 4530
16
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 Length:
Matches:
Conservative:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <UNKNOWN>
ATORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (25),568-8383
 Mismatches:
Indels:
 Sequence 1, Application US/09527487; Patent No. 6528060; GENERAL INFORMATION:
APPLICANT: NICOLETTE, Charles
TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200; CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4530
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 SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-167-322-4
 Gaps:
 LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Sequence 4, Application US/09167322 Patent No. 6365151 GENERAL INFORMATION:
 TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 83.00
88.89%
88.89%
51.88%
 TOPOLOGY: linear
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 RESULT 8
US-09-527-487-1
 Pred. No.:
 Score:
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3109 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTC 3162
 Sequence 11, Application US/09877177A

Patent No. 6582919

GENERAL INFORMATION:
APPLICANT: K. Danenberg

TITLE OF INVENTION: Method of determining Epidermal Growth

TITLE OF INVENTION: Pactor Receptor and HER2 Neu Gene Expression
TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
FILE REPERENCE: 11220/10
CURRENT APPLICATION NUMBER: US/09/877,177A

CURRENT FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 Sequence 14, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 4530
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 4530
16
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 Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
 JUNC_SEQ8_SEQ5 (1-30) x US-09-877-177A-11 (1-4530)
 ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
 Length:
Matches:
 JUNC_SEQ8_SEQ5 (1-30) x US-09-527-487-1 (1-4530)
 Indels:
 Gaps:
 ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
 83.00
88.89%
88.89%
51.88%
 83.00
88.89%
88.89%
51.88%
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Best Local Similarity:
 Georgia
 STREET: 127 Per CITY: Atlanta STATE: Georgia COUNTRY: usa
 Percent Similarity:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 US-08-229-515A-14
 US-09-877-177A-11
 US-09-877-177A-11
 LENGTH: 4530
 Query Match:
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Sequence 14, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAILUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: BEBB2 PROMOTER BINDING PROFEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: NP-LICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
CURRENT APPLICATION PARS.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/229,515A

CLASSIFICATION: 435

(TTORNEY/ACTENT)

TTORNEY/ACTENT

TTORNEY/ACTEN
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ8_SEQ5 (1-30) x US-08-229-515A-14 (1-3955)
 ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
 Gaps:
 1414.608
 ATTORNEY AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.
TELECOMMUNICATION INFORMATION:
TELEFAX: 404-688-0770
TELEFAX: 404-689-9890
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDENESS: single
 INFORMATION FOR SEQ ID NO: 14:
 81.00
100.00%
100.00%
50.62%
 SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
 404-688-9880
 TYPE: nucleic acid
STRANDEDNESS: single
 linear
 Score:
Percent Similarity:
Best Local Similarity:
 CITY: Atlanta
STATE: Georgia
 usa
 US-08-229-515A-14
 Alignment Scores:
 US-08-645-865-14
 COUNTRY:
 Query Match:
 Pred. No.:
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US-09-146-283-3
; Sequence 3, Application US/09146283
; Sequence 3, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
APPLICANT: Laus, Reiner
; APPLICANT: Ruggy, Curtis L.
APPLICANT: Ruggy, Curtis L.
; APPLICANT: Ruggy, Curtis L.
; APPLICANT: Ruggy, Curtis L.
; APPLICANT: Ruggy, Curtis L.
; APPLICANT: Ruggy, Curtis L.
; APPLICANT: Ruggy, Compositions
; CORRESPONDENCES: 10
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
 Conservative:
Mismatches:
 Conservative:
Mismatches:
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 JUNC_SEQ8_SEQ5 (1-30) x US-09-146-283-3 (1-2385)
 Matches:
 Matches:
 Length:
 Indels:
 Length:
 Indels:
 42,702
FR: 7636-0010.21
 ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION UNMBER: 7636
REFERENCE/DOCKET NUMBER: 7636
TELECHONE: 650-324-0960
TELEPHONE: 650-324-0960
 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid STRANDEDNESS: double
 81.00
100.00%
100.00%
50.62%
 0.766
68.00
66.67%
56.67%
42.50%
 STREET: 350 Cambi
CITY: Palo Alto
STATE: CA
COUNTRY: USA
; TOPOLOGY: linear
US-08-645-865-14
 linear
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 ANTI-SENSE: NO ORIGINAL SOURCE:
 ZIP: 94306
 TOPOLOGY:
 Aliqnment Scores:
 Alignment Scores:
 ORGANISM:
 Pred. No.:
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ORIGINAL SOURCE:
 ZIP: 94306
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 US-09-344-195-3
 US-09-344-195-3
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9
 RESULT 15
 Pred.
1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
 OPERATING YEAR CONSTRUCTION OPERATING STATEMENT PAPELICATION DATA:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 1976 GCACCGCCGCTCGCCCAGCCCCAGCACA 2005
 1976 GCACCGCCGCTCGCCCAGCCCCAGCACA 2005
 JUNC_SEQ8_SEQ5 (1-30) x US-08-579-823A-3 (1-2385)
 21 GlyProAla -- - SerProLeuAspSerThr 29
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
 APPLICATION NUMBER: US/08/579,823A FILING DATE: 03-DEC-1998 CLASSIFICATION: 536
 US-08-579-823A-3
; Sequence 3, Application US/08579823A
; Patent No. 6080409
 NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0860
TELEFAX: 650-324-0960
 E: Floppy disk
IBM PC compatible
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid STRANDEDNESS: double
 ATTORNEY/AGENT INFORMATION:
 66.67%
56.67%
42.50%
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Best Local Similarity:
 USA
 õ
 ORIGINAL SOURCE
 HYPOTHETICAL:
 94306
 Percent Similarity
 S
 COMPUTER:
 Alignment Scores:
 ANTI-SENSE:
 STATE: CA
 ORGANISM:
 US-08-579-823A-3
 Query Match
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 g
 δy
 δ
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ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun 1999
CLASSIFICATION: <Unknown>
 Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
 Conservative:
Mismatches:
 NAME: Judge, Linda R.
REGISTATION UNDRER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
 1976 GCACCGCCCGCTCGCCCCAGCACA 2005
 JUNC_SEQ8_SEQ5 (1-30) x US-09-344-195-3 (1-2385)
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
ATTORNEY/AGENT INFORMATION:
 21 GlyProAla --- SerProLeuAspSerThr 29
 Matches:
 Indels:
Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
Ruegg, Curtis L.
 INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
 TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
 TYPE: nucleic acid_STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
 US-08-776-251-3; Sequence 3, Application US/08776251
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS
ADDRESSEE: Dehling
 68.00
66.67%
56.67%
42.50%
 CITY: Palo Alto
 STATE: CA
COUNTRY: USA
 HYPOTHETICAL: NO ANTI-SENSE: NO
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Springer, Caroline J
APPLICANT: Springer, Caroline J
APPLICANT: Marais, Richard
SPINGER ENVERTION: Surface expression of enzyme in gene directed prodrug therapy
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vandethye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Alington
STRATE: Virginia
COMPUTER: ENP PC COMPARIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENP PC COMPARIBLE
SOCTHARE: PETENTION DATA:
ADPLICATION UNMBER: US/08/776,251
FILING DATE: 31-JAN-1997
PRIOR APPLICATION DATA:
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APPLICATION DATA:
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APPLICATION NUMBER: US/08/776,251
FILING DATE: 27-JUL-1995
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FILING DATE: AT-LING SECONOMER: 25,327
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REGISTRATION POW: 3:
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 153
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0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 JUNC_SEQ8_SEQ5 (1-30) x US-08-776-251-3 (1-153)
 EENGTH: 153 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-776-251-3
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66.00
100.00%
78.57%
41.25%
 Percent Similarity:
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 Alignment Scores:
Pred. No.:
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Search completed: October 16, 2003, 17:16:45 Job time : 16.6049 secs

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and is derived by analysis of the total score distribution

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Human cDNA for the
Human cDNA for the
Human HER-2/neu co
CDNA encoding huma
HER-2/neu oncogene
 Human Her2 antigen
Human ERBB2 DNA SE
Human Her-2/neu pr
Human Her-2/neu CD
Human Her-2/neu DD
 Human Her-2 DNA.
Her-2/neu (ERBB2/c
Human HER2 gene.
Nucleotide sequenc
Human tyrosine kin
 Human HER-2/neu pr
Human ERBB2 polynu
Human ERBB2 DNA fr
Human HER-2 CDNA.
 Human Her2/Neu enc
HER2 transgene pla
HER-2 transgene pl
Human HER2 (ErbB2)
 Human tumour antig
HER-2 nucleic acid
 Breast carcinoma r
Human HER2-neu SEQ
Human cDNA differe
 Mouse Her-2/neu cĎ
Nucleotide sequenc
Mouse Her-2/neu cD
 Human HER-2/neu on
Human heregulin 2
 Human gene express
 Human breast and o
 Human cDNA for the
 Human polynucleoti
Human HER2 (ErbB2)
 Human qene express
 Breast cancer asso
 Mouse Her-2/neu ex
 Her-2/neu extrace
 Sequence encoding cDNA encoding the
 Human cDNA for
 Description
 Mouse Her-2/neu extracellular-phosphorylation domain fusion cDNA.
 tyrosine kinase;
 Her-2/neu; oncogene; cancer; tumour; vaccine; receptor; mouse; gene therapy; gene; ss.
 ALIGNMENTS
 SUMMARIES
 ABL91709
ABK14058
 ABV78168
AAD32743
 ABQ83856
AAF24297
 AAH42210
ABA92251
 AAX01912
 AAD43935
 AAD43986
 ABA92250
 ABK10730
 AAQ46083
 AAA14812
 ABQ76220
 4BV94128
 ABK83918
 ACC50139
 ABX09987
 ABK86207
 4AZ31071
 ABN85585
 AAD43934
 Location/Qualifiers
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 17-JUN-2002 (first entry)
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Query
Match Length D
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1773
1806
3600
 4473
4530
4530
4530
4530
4530
4530
4530
 4530
 Mus musculus
 \\
 Score
 ABA92252
 RESULT 1
ABA92252
 Key
 Result
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 ; Search time 28.4941 Seconds (without alignments) 2842.104 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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| SIDSI/gcgdata/geneseqn-embl/NA1981.DAT:*
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
 5105512
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame_plus_p2n model

 160 -
1 ERGCPAEQRASPVTFQNEDLGPASPLDSTF 30
 of hits satisfying chosen parameters:
 2552756 seqs, 1349719017 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 October 15, 2003, 21:06:28
 BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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length: 2000000000
 JUNC_SEQ8_SEQ5
 Minimum DB seq
Maximum DB seq
 Title:
Perfect score:
 Scoring table:
 Total number
 OM protein
 Sequence:
 Searched:
 Database
 Run on:
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Fri

(first entry)

17-JUN-2002

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The present sequence is that of CDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) murine Her 2/neu oncoprotein (see AAM51151). The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of human cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu tusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the ECD of Her-2/neu is fused to a Her-2/neu intracellular domain or PD (or its Deltapp fragment) and minus response to Her-2/neu protein is elicited or enhanced by administering the fusion protein is elicited or enhanced by cancellular domain and delivering the transfected cells of an animal ex vivo with a nucleic acid encoding the fusion protein in and delivering the development of a specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
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/product= "Her-2/neu ECD-PD fusion"
 Conservative:
Mismatches:
Indels:
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 Length:
Matches:
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 (CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
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 Disclosure; Fig 23; 141pp; English.
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96.67%
90.00%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
 Cheever MA, Gheysen D;
 phosphorylation domain
 WPI; 2002-241743/29.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAM51152
 WO200212341-A2
 Alignment Scores:
 14-FEB-2002
 ABA92253;
 21
 Query Match:
 ..
0
 RESULT 2
 ABA92253
 Score:
 Pred.
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 SX B
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Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) and the phosphorylation domain (PD) armine Her-Z/neu oncoprotein (see AAMS)1131) plus a C-terminal TCPO motif that improves immunogenicity. The Her-Z/neu qene is amplified and the oncoprotein is overexpressed in a variety of muman cancers. Including breast, ovarian, colon, lung and prostate cancer. Her-Z/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-Z/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins, the ECD of Her-Z/neu is fused to a characterlular domain or PD (or its DeltaPD fragment). An immune response to Her-Z/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by cancer, especially breast, ovarian, collect acids encoding the fusion proteins, nucleic acids, and isolated encoding the fusion proteins, nucleic acids, and isolated concer, especially breast, ovarian, collect acids, and isolated concer, in a patient. T cells that specifically react with a Her-Z/neu cancer in a patient. T cells that specifically react with a Her-Z/neu in a sample in
 Her-2/neu extracellular-phosphorylation domain-TcP0 fusion cDNA
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; TcP0; mouse; gene therapy; gene; ss.
 Location/Qualifiers
1..2781
/*tag
/product= "Her-2/neu ECD-PD-TcP0 fusion"
 development of cancer in a patient.
 C; 779 G; 569 T; 0 other;
 2781
27
2
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Gaps:
 (CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 JUNC_SEQ8_SEQ5 (1-30) x ABA92253 (1-2781)
 Disclosure; Fig 25; 141pp; English.
 Sequence 2781 BP; 574 A; 859
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147.00
96.67%
90.00%
91.88%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507.
 - Mus musculus
- Unidentified
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 phosphorylation domain
 to inhibit the
 WPI; 2002-241743/29.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAM51153
 WO200212341-A2
 Alignment Scores:
 14-FEB-2002.
 Chimeric
 Chimeric
 Query Match:
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junc\_seq8\_seq5.rng

Alignment Scores:

Pred. No.:

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 Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antifinamatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
 New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
 Human breast and ovarian cancer associated antigen gene SEQ ID 165.
 Sequence 1115 BP; 210 A; 336 C; 338 G; 222 T; 9 other;
 cerebral anoxia and epilepsy; and infectious diseases
 1978 GGCCCCTCCAGCCCCATGGACACCTTC 2007
 21 GlyProAlaSerProLeuAspSerThrPhe 30
 Claim 1; Page 604; 1299pp; English.
 AAF21778 standard; DNA; 1115 BP.
 (HUMA-) HUMAN GENOME SCI INC.
 99US-0124270.
 08-MAR-2000; 2000WO-US05881
 (first entry)
 Rosen CA, Ruben SM;
 WPI; 2000-611515/58.
P-PSDB; AAB58875.
 WO200055173-A1.
 Homo sapiens.
 12-MAR-1999;
 27-MAR-2001
 21-SEP-2000.
 AAF21778;
 RESULT
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effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-144 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 /product="Human protein encoded by cDNA for the clone HICD_mative_coding_region"
/transl_except= (pos:1741..1752, aa:Leu-Glu)
/note= "CDS does not include stop codon"
 The invention relates to an isolated Her-2/Neu polypeptide composition
 therapy,
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;
 Novel isolated Her-2/Neu polypeptide composition useful for t
prevention and diagnosis of cancer, preferably breast cancer
1115
16
0
2
0
0
 Human cDNA for the clone HICD_native_coding_region.
 Conservative:
 Mismatches:
 Matches:
Length:
 Indels:
 Example 5; Page 118-119; 129pp; English.
 JUNC_SEQ8_SEQ5 (1-30) x AAF21778 (1-1115)
 Location/Qualifiers
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733
 83.00
88.898
88.898
51.888
 01-JUL-2002 (first entry)
 /partial
 Vedvick TS;
 (CORI-) CORIXA CORP.
 WPI; 2002-280758/32.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAE20483
 WO200214503-A2
 Homo sapiens.
 Mcneill PD,
 21-FEB-2002.
 AAD32746;
 Query Match:
 RESULT
 Score:
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```
entire Her'2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer,
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss
 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.
 preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_native_coding_region.
 /*tag= a //rtag= a //product= "Human protein encoded by cDNA for the clone HICD_CT_His_coding_region"
selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full
 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 Kalos MD;
 cancer, preferably breast cancer
 Sequence 1755 BP; 376 A; 517 C; 531 G; 331 T; 0 other;
 1755
16
0
2
0
0
 Lodes MJ,
 Human cDNA for the clone HICD_CT_His_coding_region.
 Length:
Matches:
Conservative:
 Mismatches:
 Indels:
 FOY TM,
 Example 5; Page 117-118; 129pp; English.
 JUNC_SEQ8_SEQ5 (1-30) x AAD32746 (1-1755)
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1..1764
 BP
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 14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 (first entry)
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88.89%
51.88%
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 Vedvick TS
 2002-280758/32.
 (CORI-) CORIXA CORP.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAE20481
 Hand-zimmermann
 WO200214503-A2
 Homo sapiens
 Alignment Scores:
 01-JUL-2002
 Mcneill PD,
 21-FEB-2002
 AAD32744;
 Query Match:
 RESULT
 Score:
8888888888
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 a
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preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of and other compositions for the diagnosis, prevention and treatment of patient. The invention is useful for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the caltre Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host calls. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, prophylactic or the immunotherapy of breast cancer and other Her-2/Neu associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_CT_His_coding_region.
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 /*tag= a
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 Novel isolated Her-2/New polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 30
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 Kalos MD;
 Human cDNA for the clone HICD_in_pPDM_coding_sequence.
 Sequence 1767 BP; 381 A; 521 C; 529 G; 336 T; 0 other;
 16
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 Lodes MJ,
 Conservative:
 Mismatches:
 HICD_in_pPDM_coding_sequence"
 Matches:
 Indels:
 Length:
 Foy TM,
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 Location/Qualifiers
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 AAD32747 standard; cDNA; 1773
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2000US-236428P.
2001US-270520P.
 14-AUG-2001; 2001WO-US41733.
 (first entry)
 83.00
88.89%
88.89%
51.88%
 1..1770
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 Hand-zimmermann S, Chee
Mcneill PD, Vedvick TS;
 WPI; 2002-280758/32.
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 (CORI-) CORIXA CORP
 Best Local Similarity:
 WO200214503-A2.
 Percent Similarity:
 21-FEB-2001;
 28-SEP-2000;
 Alignment Scores:
 14-AUG-2000;
 01-JUL-2002
 21-FEB-2002
 AAD32747;
 937
 Query Match:
 ..
So::
 RESULT 6
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 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the composition is useful for the therapy and diagnosis of cancer. The compositions is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of and other compositions for the diagnosis, prevention and treatment of cancer in the composition is useful for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a contine Her-2/Neu gene or gene fragments of interest, to isolate a full contine ther-2/Neu gene or gene fragments of interest, to isolate a full clength gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in complementally for the immunotherapy of breast cancer and other Her-2/Neu-contine malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_in_ppDM_coding_
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
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Matches:
Conservative:
Mismatches:
Indels:
 Human cDNA for the clone HICD_plus_8_HIS.
 JUNC_SEQ8_SEQ5 (1-30) x AAD32747 (1-1773)
 5; Page 119; 129pp; English.
 Location/Qualifiers
1..1803
 AAD32745 standard; cDNA; 1806 BP
 2000US-225152P.
2000US-236428P.
2001US-270520P.
 14-AUG-2001; 2001WO-US41733.
 83.00
88.89%
88.89%
51.88%
 01-JUL-2002 (first entry)
 0.0242
 (CORI-) CORIXA CORP
 Percent Similarity:
Best Local Similarity:
 WO200214503-A2
 14-AUG-2000;
28-SEP-2000;
21-FEB-2001;
 Homo sapiens
 Alignment Scores:
 21-FEB-2002
 sednence.
 AAD32745;
 Example
 Query Match:
 Key
 AAD32745
 RESULT
ò
 a
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```
The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of can do other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a
 polypeptide in appropriate host ceils. The composition is useful in prophylacitic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neurassociated malignancies. The invention is useful in gene therapy. The
 present sequence is human cDNA for the clone HICD_plus_8_HIS.
 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; ds.
 Kalos MD;
 Sequence 1806 BP; 391 A; 530 C; 544 G; 341 T; 0 other;
 1806
16
0
 Lodes MJ,
 Conservative:
Mismatches:
Indels:
 Location/Qualifiers
1..3600
/*tag= a /product= "HER-2/neu protein"
 Matches:
 Length:
FOY TM,
 Example 5; Page 118; 129pp; English.
 JUNC_SEQ8_SEQ5 (1-30) x AAD32745 (1-1806)
Cheever MA,
 Human HER-2/neu coding sequence.
 AAA89736 standard; DNA; 3600 BP
 12-JAN-2001 (first entry)
 83.00
88.89%
88.89%
51.88%
 Vedvick TS;
 WPI: 2002-280758/32
Hand-zimmermann S,
 Similarity:
 P-PSDB; AAE20482
 Percent Similarity:
 WO200044899-A1
 Homo sapiens.
 Mcneill PD,
 Alignment Scores:
 03-AUG-2000
 AAA89736;
 Query Match:
 Best Local
 RESULT 8
 Score:
```

junc\_seq8\_seq5.rng

bγ

```
flaviviruses and pestiviruses. The present sequence represents the coding sequence of human breast cancer antigen, Her2 variant, used as a target
 The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example tumour cells or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynucleotide (II) by a cell. This is done by administering a polynucleotide (II) exocding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and leukacemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lentiviruses (including human immunodeficiency virus (HIV)), herpesviruses and the
 Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen a cell, comprises administering a polynucleotide encoding a variant
 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
breast cancer; ovary cancer; colon cancer; lung cancer;
prostate cancer; genetic immunisation; tumour; vaccine; vector;
 Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
 Matches:
Conservative:
 Mismatches:
 (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC. (MINC/) MINCHEFF M S. (LOUK/) LOUKINOV D I.
 Indels:
 Length:
 Disclosure; Page 128-134; 146pp; English.
 the invention
 ŝ
 JUNC_SEQ8_SEQ5 (1-30) x ABK86207 (1-3678)
 Location/Qualifiers
1..3765
/*tag= b
 Zoubak
 BP
 AAT40739 standard; cDNA; 3768
 01-NOV-2001; 2001WO-US45626.
 01-NOV-2000; 2000US-0704232.
 Mincheff MS, Loukinov DI,
 (first entry)
 83.00
88.89%
88.89%
51.88%
 antigen in the method of
 WPI; 2002-527524/56.
 HER-2/neu oncogene.
 Best Local Similarity:
 (ZOUB/) ZOUBAK S.
 P-PSDB; AAU98923
 Percent Similarity:
 sapiens
 Alignment Scores:
 01-JAN-1997
 a cell, com
an antigen
 AAT40739;
 Query Match:
 Homo
 RESULT 10
 Key
 AAT40739
 g
 cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepadnavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 The present sequence encodes the human HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 /*tag= a
/product= "Breast cancer antigen Her2 variant"
 723 A; 1108 C; 1075 G; 694 T; 0 other;
 cDNA encoding human breast cancer antigen, Her2 variant.
 3600
16
0
2
0
0
 cytostatic; antiviral; immunostimulant;
 Length:
Matches:
Conservative:
Mismatches:
 Indels:
 JUNC_SEQ8_SEQ5 (1-30) x AAA89736 (1-3600)
 Location/Qualifiers
7..3678
 Disclosure; Fig 15; 128pp; English.
 BP
 ABK86207 standard; cDNA; 3678
28-JAN-2000; 2000WO-US02164.
 99US-0117976
 WPI; 2000-505976/45.
P-PSDB; AAB21198, AAB21208.
 (SMIK) SMITHKLINE BEECHAM
 (first entry)
 0.0566
83.00
88.89%
88.89%
51.88%
 Gheysen D;
 (CORI-) CORIXA CORP.
 Sequence 3600 BP;
 Best Local Similarity:
 prostate cancers
 these neoplasias
 WO200240059-A2
 Percent Similarity
 Homo sapiens
 29-JAN-1999;
 Alignment Scores:
 24-SEP-2002
 Cheever MA,
 23-MAY-2002
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Query Match:

Score Pred

ABK86207;

**ABK86207** RESULT

δ Pp Key

3678 16 0 2 0 0

junc\_seq8\_seq5.rng

```
This sequence encodes the human HER-2/\mathrm{neu} oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/\mathrm{neu} protein. The polypeptide can stimulate T cells and
 B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
 Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or
 Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
 /*tag= b
/note= "region which elicits immune response"
 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
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Mismatches:
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 Length:
Matches:
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 Claim 1a; Column 23-32; 26pp; English.
 JUNC_SEQ8_SEQ5 (1-30) x AAX01912 (1-3768)
 BP.
 AAA09455 standard; DNA; 3768
 950S-0625101.
930S-0033644.
930S-0106112.
950S-0414417.
 96US-0625101
 99WO-DK00525
 83.00
88.89%
88.89%
51.88%
 (first entry)
 UNIW) UNIV WASHINGTON
 Cheever MA, Disis ML;
 WPI; 1999-152835/13.
 preventing tumours
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAW92406
 WO200020027-A2
 Sequence 3768
 10-AUG-2000
 05-OCT-1999;
 Homo sapiens
 01-APR-1996;
17-MAR-1993;
 12-AUG-1993;
31-MAR-1995;
 Alignment Scores:
 US5869445-A.
 01-APR-1996;
 13-APR-2000.
 09~FEB-1999
 AAA09455;
 Query Match:
 RESULT 12
AAA09455
 Score:
 ò
 셤
 Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbB2) protein (AAW01111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the CDNA sequence code for the intracellular domain (Ly8676-Val1255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral
 HER-2/neu; oncogene; immune response; T cell; B cell; immunisation; malignancy; treatment; tumour; ss.
 code for
 DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
"nucleotides 2026-3765 (claim 1)
HER-2/neu intracellular domain"
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
116
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2
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0
 Conservative:
Mismatches:
Indels:
 rector, for genetic immunisation of an animal
 Length:
Matches:
 Gaps:
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/product= "HER-2/neu"
 JUNC_SEQB_SEQ5 (1-30) x AAT40739 (1-3768)
 Location/Qualifiers
1..3768
 Claim 1; Page 49-56; 71pp; English.
 /note= "oncogene"
2026..3765
 AAX01912 standard; DNA; 3768 BP
 Human HER-2/neu oncogene DNA.
 96WO-US01689
 95US-0414417
 83.00
88.898
88.898
51.888
 (first entry)
 0.0598
 (UNIW) UNIV WASHINGTON
 /note=
 Disis ML;
 WPI; 1996-455361/45.
P-PSDB; AAW01111.
 Percent Similarity:
Best Local Similarity:
Query Match:
 Homo sapiens.
 WO9630514-A1
 misc_feature
 31-MAR-1995;
 Alignment Scores:
 28-MAR-1996;
 21-APR-1999
 Cheever MA,
 03-OCT-1996
 AAX01912;
 Pred. No.:
 RESULT 11
 Key
 AAX01912
 Score:
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3768 16 0 2 0 0

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RESULT 14
 AB235744
 Score:
 Op
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 The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (1.e. self-proteins), for example, human prostate specific membrane antigen (PSM), herequin 2 (Her2) and/or fibroblast growth factor 8b (FGP8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 B-cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
 human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate, prostate, prostate, prostate, prostate, and the part of Dalum I;
 Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
 Antigen-presenting cell; immunogenic; immune response; HER-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
 Leach D,
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
 3768
116
0
2
0
0
 Haaning J,
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 /*tag= a
/product= "HER-2/neu protein"
 Gaps:
 Claim 62; Page 187-193; 220pp; English.
 Nielsen KG,
 JUNC_SEQ8_SEQ5 (1-30) x AAA09455 (1-3768)
 Human HER-2/neu protein encoding DNA
 Location/Qualifiers
 PSM, FGF8b and Her2, respectively.
 AAH23392 standard; DNA; 3768 BP.
 Mouritsen S, Niels
Birk P, Karlsson G;
 98DK-0001261.
 19-JAN-2001; 2001WO-US01850.
 (first entry)
 83.00
88.89%
88.89%
51.88%
 (MEBI-) M & E BIOTECH AS.
 WPI; 2000-349917/30.
P-PSDB; AAY92620.
 Best Local Similarity:
 WO200153463-A2
 Percent Similarity:
 Homo sapiens
05-OCT-1998;
20-OCT-1998;
 Alignment Scores:
 25-SEP-2001
 26-JUL-2001
 Steinaa L,
 Gautam A,
 AAH23392;
 Query Match:
 Pred. No.:
 RESULT 13
 AAH23392
 g
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```
The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/neu protein (also known as p185 or c-erbB2).
 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GPP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
116
0
2
0
0
 Length:
Matches:
Conservative:
Mismatches:
 á
 Hadwiger
 Indels:
 Human ERBB2 polynucleotide SEQ ID NO 52.
 JUNC_SEQ8_SEQ5 (1-30) x AAH23392 (1-3768)
 Claim 1; Page 41-46; 49pp; English
 ABZ35744 standard; DNA; 3768 BP.
 Rost S,
 Hand-Zimmermann S;
21-JAN-2000; 2000US-0177545.
 09-JAN-2001; 2001DE-1000588
 09-JAN-2001; 2001DE-1000588.
 07-FEB-2003 (first entry)
 83.00
88.89%
88.89%
51.88%
 Kreutzer R, Limmer S,
 (RIBO-) RIBOPHARMA AG
 WPI; 2001-476112/51.
 WPI; 2002-683450/74.
 (CORI-) CORIXA CORP
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAB85458
 DE10100588-A1.
 Alignment Scores:
 Homo sapiens
 18-JUL-2002.
 Cheever MA,
 ABZ35744;
 Query Match:
```

σ

```
The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (GSRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (SI, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the
 treating tumors,
hibiting expression of target genes, useful e.g. for trea introducing into cells two double-stranded RNAs that are
 Claim 13; Page 38-39; 100pp; German.
 complementary to the target
Inhibiting
 invention.
```

## Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;

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00700
 Length:
Matches:
Conservative:
Mismatches:
 Indels:
 0.0598
83.00
88.89%
88.89%
51.88%
 Best Local Similarity:
 Percent Similarity:
Alignment Scores:
 Query Match:
 ..
⊗
 Pred.
 Score
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## JUNC\_SEQ8\_SEQ5 (1-30) x ABZ35744 (1-3768)

```
2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCCATGGACAGCACCTTC 3012
13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 셤
ð
```

Search completed: October 15, 2003, 23:48:52 Job time : 32.4941 secs

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Human ERBB2 DNA fragment SEQ ID 52.
 ABX09987 standard; DNA; 3768 BP
 (first entry)
 23-JAN-2003
 ABX09987;
RESULT 15
 ABX09987
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Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.

09-JAN-2001; 2001DE-1000587. DE10100587-C1. Homo sapiens. 21-NOV-2002 

Hadwiger Rost S, Kreutzer R, Limmer S, (RIBO-) RIBOPHARMA AG

09-JAN-2001; 2001DE-1000587.

ď

Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon WPI; 2002-742209/81.

Disclosure; Page 43-44; 98pp; German

This invention describes a novel method for inhibiting expression of a target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, particularly nocogenes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (parthogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit are modified to increase their stability, ABX09936-ABX10075 represent 2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTC 3012 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30 gene fragments used to illustrate the method of the invention Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other; 0000 Conservative: Mismatches: Length: Matches: Indels: JUNC\_SEQ8\_SEQ5 (1-30) x ABX09987 (1-3768) 83.00 88.89% 88.89% 51.88% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. 222222222222222222 ò

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AX380928 Sequence
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Sequence
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 AX380942 Sequence
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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 Homo sapiens
 Percent Similarity:
Best Local Similarity:
 ø
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 937
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DEFINITION
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AX384607
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 PAT 18-MAR-2002
 PAT 18-MAR-2002
 Cheever, M.A. and Gheysen, D.
Her-2/neu fusion proteins
Patent: WO 0212341-A 28 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualifiers
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Patent: W0 0212341-A 30 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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Conservative:
Mismatches:
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 Sequence 30 from Patent W00212341. AX380944
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90.00%
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artificial sequences.
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91.88%
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Best Local Similarity:
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Compositions and methods for the therapy and diagnosis of
 Hand-Zimmermann, S., Cheever, M.A., Foy, T.M., Lodes, M.J., Kalos, M.D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Moneill, P.D. and Vedvick, T.S.

Compositions and methods for the therapy and diagnosis of her 2/neu-associated malignancies
Patent: WO 0214503-A 6 21-FEB-2002;

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 patent: WO 0240059-A 7 23-MAY-2002;
American Foundation for Biological Research Inc. (US); Mincheff,
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 PAT 29-SEP-1999
 PAT 22-JAN-2001
 1 (bases 1 to 3768)
Cheever, A. and Disis, M.L.
Methods for ellciting or enhancing reactivity to HER-2/neu protein
Patent: US 5869445-A I 09-FEB-1999;
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 Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes,M.J., Kalos,M.D., Mcneill,P.D. and Vedvick,T.S.
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Homo sapiens

ORGANISM

REFERENCE AUTHORS

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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

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 Simpson, A.J.
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profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 294)

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M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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 Simpson, A.J.
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 Score:
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Email: salmpson@ludwig.org.br
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1 (bases 1 to 337)
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-013, Sao Paulo-SP,
Shotgun sequencing of the human transcriptome with ORF expressed
 Shotgun sequencing of the human transcriptome with ORF expressed
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Fax: +55-11-2707001
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Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
EST analysis of human adipose gene expression
Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St. H4497, Baltimore, MD 21201, USA
Tel: 410 706 1622
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, ṣao Paulo-SP.
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 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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 Email: bento-soares@ulowa.edu
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CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

 (bases 1 to 423)

 Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
 Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel::319 335 8250
Fax: 319 335 9565
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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 Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (REI).
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 This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology
 No s1 sequence available.
This clone (DKRZp686M12198) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de
 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases
 MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
 Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
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 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
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Fax: +82-42-866-4409
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Xim,Y.S.
 Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea TT-El: +82-42-866-4470
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 Contact: Kim YS
Genome Research Center
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88.89%
88.89%
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PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method.
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Genome Research Center
Genome Research Center
Korea Research Institute of Bioscience & Biotechhology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South, Korea
Tel: +82-42-860-4470
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Xim,Y.S.
 30
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 Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ebeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand bothained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA libraries constructed by this method are 150 c 167 g 114 t
 BM787824 15-2002 mRNA linear EST 05-MAR-2002 K-EST0066898 S11SNU1 Homo sapiens cDNA clone S11SNU1-23-G01 5',
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 1 (bases 1 to 547)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
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Fax: +82-42-860-4409
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oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SflI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coll ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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 clone (DKFZp686M16257) is available at the RZPD in Berlin. se contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 9 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de
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D-85764 Neuherberg, GERMANY
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intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli TOP10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
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Korea Research Institute of Bioscience & Biotechnology
52 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
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library, the abundant conness in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of blotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dKfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project.
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 No si sequence available.
This clone (DKFZp686N09234) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de
 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERWANY
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GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAL03PIC1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR PAPLICATION NUMBER: 09/925,298
PRIOR PLING DATE: 2001-08-10
PRIOR PLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: FOT/VS00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
12 US-10-378-393-14

10 US-09-930-125-4

10 US-09-930-125-4

10 US-09-930-125-5

2 US-10-270-498-5

2 US-10-270-498-5

US-09-811-123-8

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US-10-422-264-29
US-09-918-995-28706
 US-09-764-869-1332
 US-09-811-123-7
US-09-811-115-1
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 NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
 1806
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3765
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 4530
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 NAME/KEY: misc_feature
LOCATION: (390)
 ORGANISM: Homo sapiens
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 SEQ ID NO 165
LENGTH: 111
 TYPE: DNA
 FEATURE:
 Sequence 165, App
 October 16, 2003, 11:08:07; Search time 31.0111 Seconds (without alignments) 2540.503 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame_plus_p2n model

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 1115 14 US-10-102-806-165
 Total number of hits satisfying chosen parameters:
 1750203 segs, 1313063994 residues
 SUMMARIES
 Listing first 45 summaries
 Published_Applications_NA:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
 Post-processing: Minimum Match 08
Maximum Match 1008
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 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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 BLOSUM62
 51.9
 Score
 Perfect score:
Sequence:
 Scoring table:
 83
 OM protein
 Searched:
 Database
 Run on:
 Result
 š
Š
 Title:
```

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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Poy, Texesa M.
APPLICANT: Foy, Texesa M.
APPLICANT: Foy, Texesa M.
APPLICANT: Michael J.
APPLICANT: Methael J.
APPLICANT: Methael D.
APPLICANT: Modvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILMS DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
Mismatches:
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 FILE REFERENCE: 210121.54
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 3.0
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 Sequence 7, Application US/09930125; Publication No. US20020193329A1
EUBLICATUNO NO. US20020193329A1
APPLICANT: Hand-Zimmerman, Susan, APPLICANT: Cheever, Martin A.
APPLICANT: Foy, Teresa M.
APPLICANT: Lodes, Michael J.
 0.00231
83.00
88.89%
88.89%
51.88%
 TYPE: DNA
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
 Best Local Similarity:
 Score:
Percent Similarity:
 Alignment Scores:
 Alignment Scores:
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 US-09-930-125-4
 US-09-930-125-7
 TYPE: DNA
 SEQ ID NO 6
 Query Match:
DB:
 Pred. No.:
 RESULT 5
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 ; Sequence 14, Application US/10378393
; Publication No. US20030182668A1
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TRANSGENIC KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378, 393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360, 889
; PRIOR PILING DATE: 2003-03-03
; SOFTWARE: Patentin version 3.2
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UG-09-930-125-6
Sequence 6, Application US/09930125
Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Edge, Michael J.
APPLICANT: Edge, Michael J.
APPLICANT: Moneill, Patricia D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS;
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
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Matches:
Conservative:
 Length:
Matches:
Conservative:
Mismatches:
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 JUNC_SEQ8_SEQ4 (1-30) x US-10-378-393-14 (1-1713)
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| LOCATION: (394)
| OTHER INFORMATION: n equals a,t,g, or c
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US-10-378-393-14
 Percent Similarity:
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 Best Local Similarity:
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 Alignment Scores:
 SEQ ID NO 14
LENGTH: 1713
 US-10-378-393-14
 Query Match:
 Query Match:
 Pred. No.:
 Pred. No.:
 RESULT 2
 ò
 ò
 Q
```

```
APPLICANT: Bol, David K.
APPLICANT: Carboni, Joan M.
APPLICANT: Rowley, Ronald B.
APPLICANT: Rowley, Ronald B.
APPLICANT: Rowley, Ronald B.
APPLICANT: Wong, Tai W.
APPLICANT: Lee, Francis Y.
TITLE OF INVENTION: TRANSCENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVAT TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
FILE REFERENCE: DO254 NP
CURRENT APPLICATION NUMBER: US/10/378,393
CURRENT FILING DATE: 2002-03-03
PRIOR FILING DATE: 2002-03-01
NUMBER OF SED ID NOS: 23
SOFTWARE: Patentin version 3.2
SED ID NO 10
LENGTH: 2411
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| Sequence 5. Application US/10207498
| Publication No. US20030143568A1
| GENERAL INFORMATION:
| APPLICANT: Elizabeth Singer
| APPLICANT: Raif Landgraf
| APPLICANT: Dennis J. Slamon
| APPLICANT: David Elsenberg
| TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
| TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
| FILE REFERENCE: 30448 1.03 4.05 4.07
| CURRENT APPLICATION NUMBER: 60/308,431
| PRIOR FILING DATE: 2001-07-27
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NOS: 24
| SEQ ID NO 5
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88.89%
88.89%
51.88%
 83.00
88.89%
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 ; LOCATION: (1)...(3765)
US-10-207-498-5
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Query Match:
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Best Local Similarity:
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 Alignment Scores:
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US-10-207-498-5
 TYPE: DNA
 TYPE: DNA
 Best Local
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 FOR THE THERAPY AND DIAGNOSIS MALIGNANCIES
 FOR THE THERAPY AND DIAGNOSIS MALIGNANCIES
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Mismatches:
Indels:
 Sequence 5, Application US/09930125
Sequence 5, Application US/09930125
Sequence 5, Application No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Codes, Michael J.
APPLICANT: Kalos, Michael D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Movelil, Patricia D.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR TITLE OF INVENTION: OP HER-2/NEU-ASSOCIATED MALE FILE REPERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
APPLICANT: Kalos, Michael D.
APPLICANT: MCMeill, Patricia D.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR:
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MAL
FILE REFRENCE: 210121:54
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTHARE: FastSEQ for Windows Version 3.0
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83.00
88.89%
88.89%
51.88%
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83.00
88.89%
88.89%
51.88%
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; ORGANISM: Homo sapiens
US-09-930-125-7
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LENGTH: 1806
TYPE: DNA
ORGANISM: Homo sapiens
US-09-930-125-5
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 Alignment Scores:
 LENGTH: 1773
 -09-930-125-5
 Query Match:
 Pred. No.:
 Pred. No.:
 RESULT
 RESULT
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2411 16 0 2 0 0

13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30

3765 16 0 2 0 0

рp

```
APPLICANT: Gheysen, Dirk
APPLICANT: Gheysen, Dirk
APPLICANT: Gheysen, Dirk
APPLICANT: Smithkilne Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
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 Sequence 9, Application US/09854356; Patent No. US2002017567Al
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
 Sequence 1, Application US/09930125; Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Hand Zimmerman, Susan
 Cheever, Martin A.
Foy, Teresa M.
Lodes, Michael J.
Kalos, Michael D.
MCNeill, Patricla D.
Vedvick, Thomas S.
 83.00
88.89%
88.89%
51.88%
 TYPE: DNA
ORGANISM: Homo sapiens
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 Percent Similarity:
 NAME/KEY: CDS
 Alignment Scores:
 RESULT 12
US-09-930-125-1
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APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT:
 FEATURE:
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 QQ
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 ð
2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCCATGGACATCCACTTT 3012
 GENERAL INCORMATION:
APPLICANT: Erickson, Sharon
APPLICANT: Sciwall, Ralph
APPLICANT: Sciwall, Ralph
APPLICANT: King, Fathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENERY. 034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
 APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENEBN: 05/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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Indels:
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Conservative:
Mismatches:
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 JUNC_SEQ8_SEQ4 (1-30) x US-09-811-115-2 (1-3768)
 Sequence 8, Application US/09811123 Patent No. US20020001587A1 GENERAL INFORMATION:
 Sequence 2, Application US/09811115
Patent No. US20020035736A1
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 83.00
88.89%
88.89%
51.88%
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88.89%
88.89%
51.88%
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; ORGANISM: Homo sapiens
US-09-811-123-8
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-811-115-2
 Percent Similarity:
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 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 Alignment Scores:
 LENGTH: 3768
 US-09-811-115-2
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Query Match:

δ qq

Pred. No.:

SEQ ID NO 2

Pred. No.:

4473 16 0 2 0 0

Conservative: Mismatches:

83.00 88.89% 51.88%

Indels:

Length: Matches:

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APPLICANT: Disis, Mary L.
APPLICANT: Helistrom, Ingegerd
APPLICANT: Helistrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
 JUNC_SEQ8_SEQ4 (1-30) x US-09-441-411-5 (1-4473)
 APPLICANT: Scholler, Nathalie B.
 ; ORGANISM: Homo sapiens US-09-441-411-5
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 LENGTH: 4473
TYPE: DNA
 US-10-101-510-81
 LENGTH: 4473
 Alignment Scores
 SEQ ID NO 81
 TYPE: DNA
 Query Match:
 Query Match:
DB:
 Pred. No.:
 RESULT 15
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES FILE REFERENCE: 210121.54 CURRENT APPLICATION NUMBER: US/09/930,125 CURRENT FILING DATE: 2001-08-14 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
 Sequence 1, Application US/10313644

Publication No. US20030157119A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
TITLE OF INVENTION: AMD VIRUS-ASSOCIATED MALIGNANCIES
FILLE REPERENCE: 210121,483C3
CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0

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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
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 JUNC_SEQ8_SEQ4 (1-30) x US-10-313-644-1 (1-3768)
 Gaps:
 US-09-441-411-5; Sequence 5, Application US/09441411; Publication No. US20030008342A1; GENERAL INFORMATION:
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83.00
88.89%
88.89%
51.88%
 0.00532
 83.00
88.89%
88.89%
51.88%
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; LOCATION: (1)...(3765)
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; LOCATION: (1)...(3765)
US-09-930-125-1
 TYPE: DNA
ORGANISM: Homo sapien
 ORGANISM: Homo sapien
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 LENGTH: 3768
 US-10-313-644-1
 TYPE: DNA
 FEATURE:
 Query Match
 Pred. No.:
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Sequence 81, Application US/10101510
| Publication No. US20030148295A1
| CENERAL INFORMATION:
| APPLICANT: WAN, JACKSON
| APPLICANT: WAN, JACKSON
| TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
| TITLE REFERENCE: 15117.0012
| CURRENT APPLICATION NUMBER: US/10/101,510
| PRIOR PELLING DATE: 2002-03-20
| PRIOR FILING DATE: 2001-03-20
| NUMBER OF SEQ ID NOS: 805
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| SOFTWARE: Patentin Ver. 2.1
 4473
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ8_SEQ4 (1-30) x US-10-101-510-81 (1-4473)
 Search completed: October 17, 2003, 03:53:11 Job time: 35.0111 secs
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83.00
88.89%
88.89%
51.88%
 ; ORGANISM: Homo sapiens US-10-101-510-81
 Percent Similarity:
Best Local Similarity:
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Sequence 25, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 2, Appli
Sequence 1, Appli
 Sequence 1, Application US/08625101
Patent No. 5869445
GENERAL INFORMATION: 586945
GENERAL INFORMATION: CHEEVER, Martin A. APPLICANT: Cheever, Mary L. TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE TITLE OF INVENTION: OR TREATUTY TO HER-2/neu PROTEIN FOR PREVENTION TITLE OF INVENTION: OR TREATUTY TO HER-2/neu FORESPONDENCE ADDRESS: ADD
 Appli
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 Sequence 430,
 Sequence 25,
Sequence 27,
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Sequence 29,
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Sequence 1
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 COMPUTER REALDED FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
 US-09-328-352-430
US-09-020-743-1
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US-08-010-347-3
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US-09-092-33-4
US-09-490-692-3
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US-09-528-911A-1
US-09-548-938A-5
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US-08-776-251-3
US-08-776-251-10
US-09-547-435-25
US-09-547-435-23
US-09-547-435-23
US-09-547-435-23
 US-09-103-840A-2
US-09-103-840A-1
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGIGSTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
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STATE: Washington
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 11, Appli
Sequence 14, Appl
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 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - nucleic search, using frame_plus_p2n model
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 US-08-625-101-1

US-08-356-786-1

US-09-048-804-1

US-09-056-105-26

US-08-229-515A-9

US-08-229-515A-9

US-09-167-322-4

US-09-167-322-4

US-09-527-487-1

US-09-229-515A-14

US-08-229-515A-14

US-08-645-865-14

US-08-645-865-14
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 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Oppermann, Hermann
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
 Testa, Hurwitz, & Thibeault STREET: Exchange Place, 53 State Street CITY: Boston STATE: Massachusetts COUNTRY: Host
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
 LOCATION: 1.3768
OTHER INFORMATION: /note= "product = "cerB-b2""
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Matches:
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 Mismatches:
Indels:
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 NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFRENCE/DOCKET NUMBER: CRP-OT TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
 Sequence 1, Application US/08356786 Patent No. 5877305
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
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83.00
88.89%
88.89%
51.88%
 TYPE: nucleic acid
STRANDEDNESS: single
 NAME/KEY: CDS
LOCATION: 1..3765
 TOPOLOGY: linear
MOLECULE TYPE: CDNA
 Percent Similarity:
Best Local Similarity:
Query Match:
 NAME/KEY: CDS
 02109
 Alignment Scores:
 US-08-625-101-1
 RESULT 2
US-08-356-786-1
 FEATURE:
 Pred. No.:
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Sequence 1, Application US/09048804

Patent No. 5968748

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA
 4473
16
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 COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,804
FILING ADTE: Herewith
CLASSIFICATION:
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Mismatches:
Indels:
 Conservative:
Mismatches:
Indels:
Length:
Matches:
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 JUNC_SEQ8_SEQ4 (1-30) x US-08-356-786-1 (1-3768)
 Matches:
 Length:
 ATTORNEY AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: 1SIS-2913
TELEPONMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 4473 base pairs
 Gaps:
 83.00
88.89% ·
88.89%
51.88%
 TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 US-09-056-105-26
 US-09-048-804-1
 US-09-048-804-1
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Alignment Scores:
 JS-08-229-515A-9
 RESULT 7
US-09-167-322-4
 Query Match
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 SERVING SON APPLICATION US/US020103

PREMERAL INFORMATION:
APPLICANT WIN YOUNG
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1999-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 4473
 Sequence 9, Application US/08229515A

Patent No. 5518885

GENERAL INFORMATION

APPLICANT: RAZIUDIN

APPLICANT: SARKAR, FAZLUL H

TITLE OF INVENTION: NEDBLA PROMOTER BINDING PROTEIN IN

TITLE OF INVENTION: NEDBLASTIC DISEASE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSED: NEDBLE & ROSENBERG PC

STREET: 127 Peachtree Street, Suite 1200
 MEDIUM TYPE: FLOPMY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
RECISTRATION NUMBER: 1414.608
FEFERENCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-0770
TELEPHONE: 404-688-0770
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 26, Application US/09056105
 LENGTH: 4530 base pairs
 83.00
88.89%
88.89%
51.88%
 TYPE: nucleic acid
STRANDEDNESS: single
 COMPUTER READABLE FORM:
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-056-105-26
 TOPOLOGY: linear
 Percent Similarity:
Best Local Similarity:
 Georgia
 CITY: Atlanta
STATE: Georgia
 usa
 ZIP: 30303
 Alignment Scores:
 US-08-229-515A-9
 COUNTRY:
 Query Match:
 ò
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APPLICANT: SARKAR, FAZIULI H
APPLICANT: SARKAR, FAZIUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPENDENCE ADDRESS:
ADDRESSE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
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 Length:
 ATTORNEY AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
 Sequence 9, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
 TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
0.00935
83.00
88.89%
88.89%
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 83.00
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88.89%
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 ; TOPOLOGY: linear
US-08-645-865-9
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 Georgia
 30303
 COUNTRY:
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Score:
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 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
 COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Sequence 4, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <UDKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
 Sequence 1, Application US/09527487
Patent No. 6528060
GENERAL INFORMATION:
APPLICANT: NICOLECTE, Charles
TITLE OF INVENTION: HERZ ANTIGENIC PEPTIDES
FILE REFERENCE: 126891309200
CURRENT APPLICATION NUMBER: US/09/527,487
UNMER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
 JUNC_SEQ8_SEQ4 (1-30) x US-09-167-322-4 (1-4530)
 APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <UNKNOWN>
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; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-167-322-4
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
INFORMATION FOR SEQ ID NO: 4:
 LENGTH: 4530 base pairs
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STRANDEDNESS: single
 SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES: 14
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88.89%
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 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
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 US-09-877-1774-11
Sequence 11, Application US/09877177A
Patent No. 6582919
GENERAL INFORMATION:
APPLICANT: K. Danenberg
TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
FILE REFERENCE: 11220/120
CURRENT APPLICATION NUMBER: US/09/877,177A
CURRENT APPLICATION NUMBER: 2001-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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 US-08-229-515A-14

Sequence 14, Application US/08229515A

Patent No. 5518885

GENERAL INFORMATION:
APPLICANT: RAZIUDIN
TITLE OF INVENTION: BRBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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127 Peachtree Street, Suite 1200
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US-09-527-487-1
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 Best Local Similarity:
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 Best Local Similarity:
 CITY: Atlanta
STATE: Georgia
COUNTRY: usa
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 ADDRESSEE:
 Alignment Scores:
 US-09-877-177A-11
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; TOPOLOGY: linear
US-08-645-865-14
 US-09-146-283-3
 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPhe 15
 APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A FILING DATE: 19 APR 1994 CLASSIFICATION: 435
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 Length:
Matches:
Conservative:
Mismatches:
 JUNC_SEQ8_SEQ4 (1-30) x US-08-229-515A-14 (1-3955)
 STREET: 127 Peachtree Street, Suite 1200 CITY: Atlanta STATE: Georgia
 Gaps:
 NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REGISTRATION NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPAX: 404-688-9880
 1414.608
 APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 14, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.
TELECOMMUNICATION INFORMATION:
TELEFAX: 404-688-0770
TELEFAX: 404-688-0880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
 INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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81.00
100.00%
100.00%
50.62%
 COMPUTER READABLE FORM:
 linear
 Percent Similarity:
Best Local Similarity:
 usa
 30303
 ; TOPOLOGY:
US-08-229-515A-14
 Alignment Scores:
 -08-645-865-14
 COUNTRY:
 Query Match:
 RESULT 11
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3955
15
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 COMPACIENT SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283 FILING DATE: 03-SEPT-1998 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
 Sequence 3, Application US/09146283
Patent No. 5976546
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene;
 Matches:
Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 JUNC_SEQ8_SEQ4 (1-30) x US-08-645-865-14 (1-3955)
 Matches:
 JUNC_SEQ8_SEQ4 (1-30) x US-09-146-283-3 (1-2385)
 Indels:
 Length:
 Length:
 3: Dehlinger & Associates
350 Cambridge Ave. Suite 250
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
 DNA (genomic)
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid STRANDEDNESS: double
 81.00
100.00%
100.00%
50.62%
 68.00
66.678
56.678
42.508
 linear
 STREET: 350 Camb
CITY: Palo Alto
STATE: CA
 Percent Similarity:
Best Local Similarity:
Query Match:
 2
 Percent Similarity:
Best Local Similarity:
Query Match:
 USA
 ORIGINAL SOURCE:
 ANTI-SENSE: NO
 MOLECULE TYPE:
HYPOTHETICAL:
 94306
 ADDRESSEE:
Alignment Scores:
 Alignment Scores:
 US-09-146-283-3
 COUNTRY:
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; Sequence 3, Application US/08776251
 HYPOTHETICAL: NO ANTI-SENSE: NO
 ORIGINAL SOURCE:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 US-09-344-195-3
 US-08-776-251-3
 US-09-344-195-3
 Query Match:
 Pred. No.:
 RESULT 15
 ŏ
 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongy,
TITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 Length:
Matches:
Conservative:
 Mismatches:
 1976 GCACCCGCCCCCCAGCCCCAGCACA 2005
 1976 GCACCGCCGCTCGCCCAGCCCCAGCACA 2005
 JUNC_SEQ8_SEQ4 (1-30) x US-08-579-823A-3 (1-2385)
 21 GlyProAla --- SerProLeuAspSerThr 29
 21 GlyProAla --- SerProLeuAspSerThr 29
 Indels:
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
 ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010
TELECOMMUNICATION:
TELEPHONE: 650-324-0880
 APPLICATION NUMBER: US/08/579,823A FILING DATE: 03-DEC-1998 CLASSIFICATION: 536
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 3, Application US/08579823A Patent No. 6080409
 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
 TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
 66.678
56.678
42.508
 TYPE: nucleic acid
STRANDEDNESS: double
 linear
 Percent Similarity:
Best Local Similarity:
 USA
 ANTI-SENSE: NO ORIGINAL SOURCE:
 94306
 Š
 Alignment Scores:
 ORGANISM:
 RESULT 13
US-08-579-823A-3
 US-08-579-823A-3
 STATE: C
COUNTRY:
 Query Match:
 Score:
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ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 Ruegg, Curtis L.

Wu, Hongyu

TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENS: 20
CORRESPONDENS: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
 Conservative:
Mismatches:
 NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
 1976 GCACCCGCCCGCTCGCCCAGCACA 2005
 JUNC_SEQ8_SEQ4 (1-30) x US-09-344-195-3 (1-2385)
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
CLASSIFICATION: <UNKNOWN>
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
 21 GlyProAla---SerProLeuAspSerThr 29
 Length:
 Indels:
Sequence 3, Application US/09344195 Patent No. 6210662 GENERAL INFORMATION:
 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
 ATTORNEY/AGENT INFORMATION:
 TYPE: nucleic acid
STRANDEDNESS: double
 COUNTRY: USA ZIP: 94306 COMPUTER READABLE FORM:
 APPLICANT: Laus, Reiner
 68.00
66.67%
56.67%
42.50%
 CITY: Palo Alto
```

```
GENERAL INFORMATION:
GREEAL INFORMATION:
GREEAL INFORMATION:
SPELICARY: Springer, Caroline J
SPELICARY: Marias, Richard
TITLE OF INVERTION: Surface expression of enzyme in gene directed prodrug therapy
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vandenhye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
STRATE: Virgina
COUNTRY: USA
COMPUTER: Eloppy disk
COMPUTER: The PORM:
WEDING TIME STREET: PORMS:
MEDING THE PROPHY OF THE STREET PROPHY:
SOFTWARE: PROPHY OF THE STREET PROPHY:
APPLICATION NUMBER: USA OF THE STREET STRE
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ8_SEQ4 (1-30) x US-08-776-251-3 (1-153)
 Gaps:
 0.0516
66.00
100.00%
78.57%
41.25%
 ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-776-251-3
 Score:
Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
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Search completed: October 16, 2003, 17:16:36 Job time : 16.6049 secs THIS PAGE BLANK (USPTO)

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Human breast and o
Human CDNA for the
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 CDNA encoding huma
HER-2/neu oncogene
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Human ERBB2 Dolynu
 Human Her2 antigen
Human ERBB2 DNA SE
Human Her-2/neu pr
Human Her-2/neu cb
Human Her-2/neu bN
Human polynucleoti
Human HER2 (ErbB2)
 Sequence encoding
CDNA encoding the
Human tumour antig
HER-2 nucleic acid
 Human Her2/Neu enc
HER2 transgene pla
HER-2 transgene pl
Human HER2 (ErbB2)
 Her-2/neu (ERBB2/c
Human HER2 gene.
 Nucleotide sequenc
Human tyrosine kin
Human gene express
 Breast carcinoma r
Human HER2·neu SEQ
Human cDNA differe
 Mouse Her-2/neu cD
Nucleotide sequenc
Mouse Her-2/neu cD
 Human gene express
Human Her-2 DNA.
 Mouse Her-2/neu ex
 Human HER-2 cDNA.
 Breast cancer asso
 Description
 Mouse Her-2/neu extracellular-phosphorylation domain fusion cDNA.
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; mouse; gene therapy; gene; ss.
and is derived by analysis of the total score distribution.
 ALIGNMENTS
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ABK10730
ABL91709
ABK14058
AAQ46083
AAA14812
 ABQ76220
AAZ31071
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ABA92251
 ABZ34969
 ABV94128
ABN85585
 AAX01912
 AAD43986
 ABA92252
 ABV78168
 AAD32743
 AAD38904
 AAD43934
 AAD4393
 AAD1973
 Location/Qualifiers
1..2763
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 DB
 17-JUN-2002 (first entry)
 Query
Match Length
 11115
1755
1767
1773
1806
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3678
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 Mus musculus.
 Score
 Key
 RESULT 1
 ABA92252
 Result
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 (without alignments)
2842.104 Million cell updates/sec
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| SIDSI/gcgdata/geneseqn.embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1986.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1986.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn.embl/NA1980.DAT:*
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
 October 15, 2003, 21:06:28; Search time 28.4941 Seconds
 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame_plus_p2n model

 1 ERGCPAEQRASPVTFONEDLGPASPLDSTF 30
 hits satisfying chosen parameters:
 2552756 seqs, 1349719017 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 BLOSUM62
Xgapop 10.0, Xgapext (
Ygapop 10.0, Ygapext |
Fgapop 6.0, Fgapext |
Delop 6.0, Delext
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 JUNC_SEQ8_SEQ4
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 οĘ
 Title:
Perfect score:
 Scoring table:
 Total number
 OM protein
 Sequence:
 Searched:
 Database
 Run on:
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Her-2/neu extracellular-phosphorylation domain-TcPO fusion cDNA Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; TcP0; mouse; gene therapy; gene; ss.

(first entry)

17-JUN-2002

/product= "Her-2/neu ECD-PD-TcP0 fusion"

Location/Qualifiers 1..2781 /\*tag= a

- Mus musculus - Unidentified

Chimeric Chimeric

(CORI-) CORIXA CORP. (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Cheever MA, Gheysen D;

WPI; 2002-241743/29. P-PSDB; AAM51153.

03-AUG-2001; 2001WO-US24283. 03-AUG-2000; 2000US-0632507.

WO200212341-A2

14-FEB-2002.

```
The presult sequence is that on the phosphorylation domain (PD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAM51151). The Her-2/neu gene is multine Her-2/neu oncoprotein (see AAM51151). The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of fumban cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu cancer. Her-2/neu ovarian cancers. The invention provides Her-2/neu fusion proteins, the ECD of Her-2/neu is fused to a Her-2/neu intracellular domain or PD (or its DeltapD fragment). An excines comprising the fusion protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid emcoding the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid colon, the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in corder to inhibit the development of cancer in a patient.
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 The present sequence is that of cDNA encoding a fusion between
 571 A; 855 C; 772 G; 565 T; 0 other;
 /*tag= a
/product= "Her-2/neu ECD-PD fusion"
 Length:
Matches:
Conservative:
 Mismatches:
Indels:
 1978 GGCCCCTCCAGCCCCATGGACACCTTC 2007
 21 GlyProAlaSerProLeuAspSerThrPhe 30
 (CORI-) CORIXA CORP. (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Gaps:
 JUNC_SEQ8_SEQ4 (1-30) x ABA92252 (1-2763)
 Disclosure; Fig 23; 141pp; English.
 ABA92253 standard; cDNA; 2781
 1.96e-11
147.00
96.67%
90.00%
91.88%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
 Cheever MA, Gheysen D;
 phosphorylation domain
 WPI; 2002-241743/29.
 Sequence 2763 BP;
 Best Local Similarity:
 P-PSDB; AAM51152
 WO200212341-A2
 Percent Similarity:
 Alignment Scores:
 14-FEB-2002
 ABA92253;
 Query Match:
 RESULT 2
 ABA92253
δ
 셤
 δ
 g
```

```
Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAMS1131) plus a C-terminal TCPO motif that improves immunogenicity. The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of human cancers. Including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the ECD of Her-2/neu intracellular domain or PD (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by conding the fusion protein in the form of a vaccine, or by conding the fusion protein, nucleic acids, and isolated encoding the fusion protein, nucleic acids, and isolated concern the animal. The fusion protein, nucleic acids, and isolated concern concern the animal. The fusion protein is elicited or engaged cells of the fusion protein, nucleic acids, and isolated cancer, especially presst, ovarian, colon, lung or protein encorrer in a patient. T cells that specifically react with a Her-2/neu fusion protein concerned in a patient. T cells that specifically react with a Her-2/neu
 order to inhibit the development of cancer in a patient.
 Sequence 2781 BP; 574 A; 859 C; 779 G; 569 T; 0 other;
 Conservative:
Mismatches:
Indels:
 Matches:
 Length:
 Disclosure, Fig 25; 141pp; English.
 1.97e-11
 147.00
96.67%
90.00%
91.88%
 phosphorylation domain
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Query Match:
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JUNC\_SEQ8\_SEQ4 (1-30) x ABA92253 (1-2781)

m

```
Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are proteins AAB58711 - AAB59128. The DNA and protein sequences are sascoitated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AB59129 which are used in the invention and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic, neuroprotective; antivital; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidabetic; antiparasitic and cardiant activity. The cylubacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis, proteins, agonists and agonists may also be used in the diagnosis, proteins, agonists and agonists may also be used in the diagnosis, proteins and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as myocardial anoxia and epilepsy; and infectious diseases.
New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
 Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autofimune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rhemmatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
 Human breast and ovarian cancer associated antigen gene SEQ ID 165.
 GlyProAlaSerProLeuAspSerThrPhe 30
 Claim 1; Page 604; 1299pp; English.
 BP
 AAF21778 standard; DNA; 1115
 (HUMA-) HUMAN GENOME SCI INC.
 99US-0124270.
 08-MAR-2000; 2000WO-US05881.
 (first entry)
 WPI; 2000-611515/58.
 Rosen CA, Ruben SM;
 P-PSDB; AAB58875
 WO200055173-A1.
 Homo sapiens.
 12-MAR-1999;
 27-MAR-2001
 21-SEP-2000.
 1978
 AAF21778;
 RESULT 3
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Sequence 1115 BP; 210 A; 336 C; 338 G; 222 T; 9 other;

```
The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 "Human protein encoded by cDNA for the clone
 Novel isolated Her-2/New polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 onn S, Cheever MA, Foy TM, Lodes MJ, Kalos MD; Vedvick TS;
 / Lus

/ Product= "Human process:

HICD_native_coding_region"

/transl_except= (pos:1741..1752, aa:Leu-Glu)

/note= "CDS does not include stop codon"
 1115
16
0
2
0
0
 Human cDNA for the clone HICD_native_coding_region.
 Conservative:
 Mismatches:
Indels:
 Matches:
 Length:
 Example 5; Page 118-119; 129pp; English.
 JUNC_SEQ8_SEQ4 (1-30) x AAF21778 (1-1115)
 Location/Qualifiers
1..1755
 AAD32746 standard; cDNA; 1755 BP
 14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733.
 01-JUL-2002 (first entry)
 83.00
88.89%
88.89%
51.88%
 ๙
 /*tag=
 WPI; 2002-280758/32.
 (CORI-) CORIXA CORP
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAE20483
 Hand-zimmermann
 WO200214503-A2
 Homo sapiens.
Alignment Scores:
 Mcneill PD,
 21-FEB-2002
 AAD32746;
 Query Match:
 ..
9
 RESULT
```

```
entire Her-2/New gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_native_coding_region.
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.
 /*tag= a
/product= "Human protein encoded by cDNA for the clone
HICD_CT_His_coding_region"
form duplex molecules with complementary stretches of the 2/Neu gene or gene fragments of interest, to isolate a full
 isolated Her-2/Neu polypeptide composition useful for therapy, ntion and diagnosis of cancer, preferably breast cancer
 30
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 Kalos MD;
 Sequence 1755 BP; 376 A; 517 C; 531 G; 331 T; 0 other;
 1755
16
0
2
0
0
 Foy TM, Lodes MJ,
 Human cDNA for the clone HICD_CT_His_coding_region.
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Example 5; Page 117-118; 129pp; English.
 JUNC_SEQ8_SEQ4 (1-30) x AAD32746 (1-1755)
 Location/Qualifiers
1..1764
 BP.
 Cheever MA,
 AAD32744 standard; cDNA; 1767
 14-AUG-2001; 2001WO-US41733.
 2000US-225152P
 28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 (first entry)
 0.0239
83.00
88.89%
88.89%
51.88%
 Vedvick
 2002-280758/32.
 (CORI-) CORIXA CORP
 Hand-zimmermann S,
 Percent Similarity:
Best Local Similarity:
Query Match:
 WPI; 2002-280758/
P-PSDB; AAE20481.
 WO200214503-A2
 prevention and
 Homo sapiens
 14-AUG-2000;
 Alignment Scores:
 01-JUL-2002
 Mcneill PD,
 21-FEB-2002
 AAD32744;
 937
 No.:
 Novel
 RESULT
 Score:
 Pred.
 8888888888888
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 g
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preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in preferably for the immunotherapy of Dreast cancer and other Her-2/Neu associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_CT_His_coding_region.
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytoskatic; gene; ss
 /product= "Human protein encoded by cDNA for the clone
HICD_in_pPDM_coding_sequence"
 Novel isolated Her-2/New polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 composition is useful for the therapy and diagnosis of cancer,
 Kalos MD;
 Human cDNA for the clone HICD_in_pPDM_coding_sequence.
 Sequence 1767 BP; 381 A; 521 C; 529 G; 336 T; 0 other;
 Lodes MJ,
 0 0 0 0 0
 Length:
Matches:
Conservative:
Mismatches:
 Indels:
 Cheever MA, Foy TM,
 JUNC_SEQ8_SEQ4 (1-30) x AAD32744 (1-1767)
 Location/Qualifiers
1..1770
 BP.
 AAD32747 standard; cDNA; 1773
 2000US-225152P.
2000US-236428P.
2001US-270520P.
 14-AUG-2001; 2001WO-US41733
 /*tag= a
/product= '
 (first entry)
 0.0241
83.00
88.89%
88.89%
51.88%
 Hand-zimmermann S, Chee
Mcneill PD, Vedvick TS;
 WPI; 2002-280758/32.
P-PSDB; AAE20484.
 (CORI-) CORIXA CORP.
 Best Local Similarity:
 WO200214503-A2
 Percent Similarity:
 Homo sapiens
 14-AUG-2000;
 21-FEB-2001;
 28-SEP-2000;
 Alignment Scores:
 01-JUL-2002
 21-FEB-2002
 AAD32747;
 Query Match:
 RESULT 6
 AAD32747
g
```

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03-AUG-2000
 AAA89736;
 Query Match:
 Best Local
 RESULT 8
 AAA89736
 Score:
 8 X C C C C C C C C C C C C C C X B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X X B B X B X B X B B X B B X B B X B B X B B X B B X B B X B X B B X B X B B X B B X B B X B X B B X B B X B X B B X B X B B X B X B B X B X B X B X B B X
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 q
 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The career, in pharmaceutical compositions, e.g., vaccine prefarably breast cancer, in pharmaceutical compositions, e.g., vaccine numan malignancies, for stimulating and/or expanding T cells specific for therapy and diagnosis of cancer in a patient. The invention is useful for stimulating at Cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centre Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a length gene from a suitable library, and to direct expression of a polygeptide in appropriate host cells. The composition is useful in
 prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neurassociated mailgnancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_in_pPDM_coding_
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 /product= "Human protein encoded by cDNA for the clone HICD_plus_8_HIS"
 /transl_except= (pos:1543..1545, aa:Pro)
 1773
16
0
2
0
0
 Sequence 1773 BP; 383 A; 528 C; 530 G; 332 T; 0 other;
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Human cDNA for the clone HICD_plus_8_HIS
 JUNC_SEQ8_SEQ4 (1-30) x AAD32747 (1-1773)
 Example 5; Page 119; 129pp; English.
 Location/Qualifiers
 AAD32745 standard; cDNA; 1806 BP
 14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733.
 83.00
88.89%
88.89%
51.88%
 01-JUL-2002 (first entry)
 ø
 /*tag=
 1.1803
 (CORI-) CORIXA CORP
 Similarity:
 Percent Similarity:
Best Local Similari
 WO200214503-A2
 Homo sapiens.
 Alignment Scores:
 21-FEB-2002
 sednence.
 AAD32745;
 Query Match:
 Key
 RESULT 7
 AAD32745
 Score:
\overset{\times}{\times}
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effective for electring an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HIA)-144 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of modern cand other compositions for the diagnosis, prevention and treatment of thuman malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a real response in a contine Her-2/Neu gene or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centure Her-2/Neu gene or gene fragments of intect expression of a colypeptide in appropriate host cells. The composition is useful in preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_plus_B-HIS.
 The invention relates to an isolated Her-2/Neu polypeptide composition
 therapy,
 Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; ds.
Kalos MD;
 Novel isolated Her-2/Neu polypeptide composition useful for t
prevention and diagnosis of cancer, preferably breast cancer
 Sequence 1806 BP; 391 A; 530 C; 544 G; 341 T; 0 other;
 1806
16
0
2
0
0
Lodes MJ,
 Conservative:
Mismatches:
Indels:
 /*tag= a
/product= "HER-2/neu protein"
 Length:
Matches:
FOY TM,
 Gaps:
 JUNC_SEQ8_SEQ4 (1-30) x AAD32745 (1-1806)
 Example 5; Page 118; 129pp; English.
 Location/Qualifiers
Cheever MA,
 Human HER-2/neu coding sequence.
 BP.
 AAA89736 standard; DNA; 3600
 12-JAN-2001 (first entry)
 83.00
88.89%
88.89%
51.88%
 Vedvick TS;
 1..3600
 WPI; 2002-280758/32.
Hand-zimmermann S,
 Similarity:
 P-PSDB; AAE20482
 Percent Similarity:
 WO200044899-A1
 Alignment Scores:
 Homo sapiens
 Mcneill PD,
```

29-JAN-1999;

Cheever MA,

by of

prostate cancers -

```
The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example timnour cells, or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynuclectide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pencreatic cancer, as well as lymphomas and leukaemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lentiviruses (including human immunodeficiency virus (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present sequence represents the coding sequence of human breast cancer antigen, Her2 variant, used as a target antigen in the method of the invention.
 Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen a cell, comprises administering a polynucleotide encoding a variant of
 2869 GTGGTCATCCAGAATGAGGACTTGGGCCCAGTCCCTTGGACAGCACCTTC 2922
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
 breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
 Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
 Conservative:
Mismatches:
 Length:
Matches:
 AMERICAN FOUND BIOLOGICAL RES INC.
MINCHEFF M S.
LOUKINOV D I.
 Indels:
 Disclosure; Page 128-134; 146pp; English.
 ŝ
 JUNC_SEQ8_SEQ4 (1-30) x ABK86207 (1-3678)
 Location/Qualifiers
1..3765
/*tag= b
 Zoubak
 BP
 AAT40739 standard; cDNA; 3768
 01-NOV-2001; 2001WO-US45626.
 01-NOV-2000; 2000US-0704232.
 DI,
 0.0581
83.00
88.89%
88.89%
51.88%
 (first entry)
 Mincheff MS, Loukinov
 WPI; 2002-527524/56.
P-PSDB; AAU98923.
 HER-2/neu oncogene.
 Best Local Similarity:
 ZOUBAK S
 Percent Similarity
 Alignment Scores:
 sapiens
 01-JAN-1997
 AAT40739;
 (LOUK/)
 (AMBI-)
 (MINC/)
 Query Match:
 Homo
 Key
 GI.
 ò
 Human; Her2; cytostatic; antiviral; immunostimulant; cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepadnavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 The present sequence encodes the human HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 "Breast cancer antigen Her2 variant"
 723 A; 1108 C; 1075 G; 694 T; 0 other;
 cDNA encoding human breast cancer antigen, Her2 variant.
 3600
116
0
0
0
 Length:
Matches:
Conservative:
 Mismatches:
Indels:
 JUNC_SEQ8_SEQ4 (1-30) x AAA89736 (1-3600)
 Location/Qualifiers 7..3678
 Disclosure; Fig 15; 128pp; English.
 ABK86207 standard; cDNA; 3678 BP.
28-JAN-2000; 2000WO-US02164.
 99US-0117976
 (CORI-) CORIXA CORP.
 /rtag= a
/product= '
 P-PSDB; AAB21198, AAB21208
 83.00
88.89%
88.89%
51.88%
 (first entry)
 Gheysen D;
 WPI; 2000-505976/45
```

Sequence 3600 BP;

Alignment Scores:

.. No.:

Score: Pred

these neoplasias

Similarity:

Query Match:

Percent Similarity:

WO200240059-A2

23-MAY-2002

Homo sapiens

24-SEP-2002

RESULT 9 ABK86207

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3678 116 0 2 0 0

junc\_seq8\_seq4.rng

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```
This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing
 Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or
 Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
 "region which elicits immune response"
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 tumour, or to prevent tumour occurrence or reoccurrence
 Conservative:
Mismatches:
 Matches:
 Length:
 Indels:
 Human heregulin 2 (Her2) coding sequence.
 Claim la; Column 23-32; 26pp; English.
 JUNC_SEQ8_SEQ4 (1-30) x AAX01912 (1-3768)
 BP.
 DNA: 3768
 96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
 96US-0625101
 99WO-DK00525
 0.0598
83.00
88.89%
88.89%
51.88%
 (first entry)
 /*tag=
/note=
 (UNIW) UNIV WASHINGTON
 Disis ML;
 WPI; 1999-152835/13.
 preventing tumours
 AAA09455 standard;
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAW92406
 WO200020027-A2
 01-APR-1996;
17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
 Cheever MA,
 10-AUG-2000
 05-OCT-1999;
 Alignment Scores:
 US5869445-A.
 09-FEB-1999.
 01-APR-1996;
 13-APR-2000.
 AAA09455;
 Query Match:
 No.:
 Ношо
 AAA09455
 RESULT
 Score:
 Pred.
 Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbB2) protein (AAW01111). The oncogene is overexpressed in various
 cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the CDNA sequence odde for the intracellular domain (Ly8676-Val1255) of the HBR-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral vector, for genetic immunisation of an animal.
 HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
malignancy; treatment; tumour; ss.
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
/note= "nucleotides 2026-3765 (claim 1) code for
HER-2/neu intracellular domain"
 DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
16
0
2
0
0
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Location/Qualifiers
1..3768
/*tag= a
/product= "HER-2/neu"
 JUNC_SEQ8_SEQ4 (1-30) x AAT40739 (1-3768)
 Claim 1; Page 49-56; 71pp; English.
 /note= "oncogene"
2026..3765
 AAX01912 standard; DNA; 3768 BP
 Human HER-2/neu oncogene DNA.
 96WO-US01689
 95US-0414417
 0.0598
83.00
88.89%
88.89%
 (first entry)
 (UNIW) UNIV WASHINGTON
 Disis ML;
 WPI; 1996-455361/45.
P-PSDB; AAW01111.
 Percent Similarity:
Best Local Similarity:
 WO9630514-A1
 Homo sapiens.
 28-MAR-1996;
 31-MAR-1995;
 Alignment Scores:
 misc_feature
 21-APR-1999
 Cheever MA,
 03-OCT-1996
 associated
 AAX01912;
 Query Match:
 ..
0
 RESULT 11
 AAX01912
 Score:
 Pred.
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3768 16 0 2 0 0

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junc\_seq8\_seq4.rng

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AB235744
 The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (1.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
 human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human
 Dalum I;
 2959 GIGGTCATCCAGAATGAGGACTTGGGCCCAGCCAGCCCTTGGACAGCACCTTC 3012
 Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
 Antigen-presenting cell; immunogenic; immune response; HER-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 Nielsen KG, Haaning J, Leach D,
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
 3768
116
0
2
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 /*tag= a
/product= "HER-2/neu protein"
 Claim 62; Page 187-193; 220pp; English.
 Human HER-2/neu protein encoding DNA
 JUNC_SEQ8_SEQ4 (1-30) x AAA09455 (1-3768)
 Location/Qualifiers
1..3768
/*tag= a
 to treat prostate, prostate/breast SSM, FGF8b and Her2, respectively.
 BP.
 Mouritsen S, Nielse
Birk P, Karlsson G;
 AAH23392 standard; DNA; 3768
98DK-0001261.
98US-0105011.
 19-JAN-2001; 2001WO-US01850
 83.00
88.898
88.898
51.888
 (first entry)
 (MEBI-) M & E BIOTECH AS.
 2000-349917/30.
 Best Local Similarity:
 P-PSDB; AAY92620
 WO200153463-A2
 Percent Similarity:
05-OCT-1998;
20-OCT-1998;
 Homo sapiens
 Alignment Scores:
 25-SEP-2001
 26-JUL-2001
 Steinaa L,
 Gautam A,
 AAH23392;
 Query Match:
 Pred. No.:
 RESULT 13
 Key
 AAH23392
 Score:
οy
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The invention provides an isolated antigen-presenting ceil, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/neu protein (also known as pl85 or c-erbB2).
 Double stranded RNA; dsRNA; RNAI; RNA inhibition; cytostátic; virucide; profezoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/new protein, particularly useful for treating or preventing cancer, e.g. breast cancer
 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 Length:
Matches:
Conservative:
Mismatches:
 <u>ا</u>
 Hadwiger
 Indels:
 Human ERBB2 polynucleotide SEQ ID NO 52.
 JUNC_SEQ8_SEQ4 (1-30) x AAH23392 (1-3768)
 Claim 1; Page 41-46; 49pp; English
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 BP.
 Hand-Zimmermann S;
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21-JAN-2000; 2000US-0177545.
 39-JAN-2001; 2001DE-1000588.
 09-JAN-2001; 2001DE-1000588
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83.00
88.89%
88.89%
 07-FEB-2003 (first entry)
 Kreutzer R, Limmer S,
 (RIBO-) RIBOPHARMA AG
 (CORI-) CORIXA CORP.
 WPI; 2001-476112/51.
 WPI; 2002-683450/74.
 Best Local Similarity:
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 Percent Similarity:
 DE10100588-A1
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 Cheever MA,
 18-JUL-2002
 ABZ35744;
 Query Match:
 RESULT 14
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for treating tumors,
Inhibiting expression of target genes, useful e.g. for trea' by introducing into cells two double-stranded RNAs that are
 Claim 13; Page 38-39; 100pp; German.
 complementary to the target
```

The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (GSRNAI and II), both with a double-stranded (4s) structure of at most 49 sequential nucleotide pairs. At least part of one strand (51, \$2) of the ds structures in each of dssRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by prefreating the cells with interferon. The present sequence is that of a target DNA of the Invention

Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;

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3768
16
0
2
0
0
 Matches:
Conservative:
Mismatches:
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Search completed: October 15, 2003, 23:48:48 Job time: 31.4941 secs

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 ABX09987 standard; DNA; 3768 BP
 (first entry)
 23-JAN-2003
 ABX09987;
RESULT 15
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Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.

DE10100587-C1. Homo sapiens 21-NOV-2002 09-JAN-2001; 2001DE-1000587 (RIBO-) RIBOPHARMA AG

09-JAN-2001; 2001DE-1000587.

Rost S, Hadwiger P;

WPI; 2002-742209/81.

Kreutzer R, Limmer S,

δ Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon

Disclosure; Page 43-44; 98pp; German

```
This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsnN1) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsnNaI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, id (not defined) to protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasamodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsnNa can inhibit interferon greatly increases their stant the effect is even greater when dsnNa care modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention.
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
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Conservative:
 Mismatches:
 Length:
 Indels:
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88.89%
88.89%
51.88%
 Similarity:
 Percent Similarity:
 Alignment Scores:
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 Best Local
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 Score:
 Pred.
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AB096613 Homo sapi
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Sequence
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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 Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes,M.J., Kalos,M.D., Mcneill,P.D. and Vedvick,T.S. Compositions and methods for the therapy and diagnosis of
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Compositions and methods for the therapy and diagnosis of her-2/neu-associated malignancies
Patent: WO 0214503-A 6 21-FEB-2002;
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 Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes,M.J., Kalos,M.D.,
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Compositions and methods for the therapy and diagnosis of
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Homo sapiens
 Homo sapiens (human)
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 Patent: WO 0240059-A 7 23-MAY-2002;
Patentican Foundation for Biological Research Inc. (US); Mincheff,
Milcho S. (US); Loukinov, Dmitri I. (US); Zoubak, Serguei (US)
Location/Qualifiers
 Mincheff,M.S., Loukinov,D.I. and Zoubak,S. Methods and compositions for inducing cell-mediated immune
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 FEATURES
 ORIGIN
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 PAT 29-SEP-1999
 PAT 22-JAN-2001
 1 (bases 1 to 3768)
Cheever, A. and Disis, M.L.
Wethods for ellciting or enhancing reactivity to HER-2/neu protein
Patent: US 5869445-A I 09-FEB-1999;
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 Erickson,S. and Schwall,R.
Methods of treatment using anti-erbb antibody-maytansinoid
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1171 c 1119 g 719 t
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1171 c 1119 g 719 t
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 13 ValThrPheGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Gaiger, A., Cheever, M.A. and Hand-Zimmermann, S. Methods for diagnosis and therapy of hematological and virus-associated malignancies
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LL6in10025T7 AFT024-subtracted library Mus musculus cDNA 5' similar to New/ERBB-2 p185, mRNA sequence.
 Contact: Moore, Kateri A.
Department of Molecular Biology
Princeton University
217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Hackney, J.A., Charbord, P., Brunk, B.P., Stoeckert, C.J., Lemischka, J.R. and Moore, R.A.
A. molecular profile of a hematopoietic stem cell niche
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)
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 Fax: 609 258 2759
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 University of Iowa 375 MEBRF, Iowa City, IA 52242, USA 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at Seq primer: M13 Forward.
 been derived was used as a driver in a hybridization with
the pooled UI-R-Al and UI-R-El library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
 hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
 Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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Email: kmoore@molblo.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for
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Seq primer: MI3Reverse or T7.
Location/Qualifiers
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 Tel: 609 258 0605
Fax: 609 258 2759
Email: kmoore@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for
gene products expressed by a hematopoietic stem cell-supporting
stromal call line, AFT024.
Seq primer: M13Reverse or T7.
Location/Qualifiers
 beta-actin and enriched for transcripts specific to
AFT024. For detailed protocols and additional information
please see our website at
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 577)
 Hackney, J. A., Charbord, P., Brunk, B. P., Stoeckert, C. J., Lemischka, I. B. and Moore, K. A.
A molecular profile of a hematopoietic stem cell niche
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)
 2 others
 http://stromalcell.princeton.edu."
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 Contact: Moore, Kateri A.
Department of Molecular Biology
 Mus musculus (house mouse)
Mus musculus
 Contact: Moore, Kateri
 Princeton University
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Hackney,J.A., Charbord,P., Brunk,B.P., Stoeckert,C.J., Lemischka,I.R. and Moore,K.A.
A molecular profile of a hematopoietic stem cell niche Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)
 217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
 Rattus norvegicus (Norway rat)
Sattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Conservative:
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Indels:
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 Contact: Moore, Kateri A.
Department of Molecular Biology
Princeton University
 Mus musculus (house mouse)
Mus musculus
 Contact: Dan Fitzpatrick
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transcribed from the driver, 2018 cDNA library in pSport2
with inserts cloned in the complementary orientation. The
AFT024-subtracted library contains 4.2x105 clones and is
depleted of common housekeeping gene products eg.
beta-actin and enriched for transcripts specific to
AFT024. For detailed protocols and additional information
please see our website at
http://stromalcell.princeton.edu."
 DESGLUGS 592 bp MRNA linear EST 21-JUL-2000 601272225F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3601422 5',
 Email: kmoore@molbio.princeton.edu
These ESTS are derived from a subtracted cDNA library enriched for
gene products expressed by a hematopoietic stem cell-supporting
stromal cell line, AFT024.
217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
 Mus musculus (house mouse)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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 Contact: Robert Strausberg, Ph.D.
Baal: cgapbs-remail.nih.gov
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Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
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Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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Site_2: Not I; The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNW was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous
 EST 26-AUG-2002
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
This clone was contributed by the Brain Molecular Anatomy Project
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 715)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
from 11 wk male, 7 days post-castration, average insert size 2.5 kb). Constructed by Life
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 Length:
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 Mus musculus (house mouse)
Mus musculus
 BU052728.1 GI:22492805
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88.89%
88.89%
52.17%
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Outpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Reference for transgenic model: Xu et al., Nature Genetics
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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 Unpublished
Contact: Robert Strausberg, Ph.D.
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Mus musculus
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 Email: cgapbs-remainin.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: Limilingov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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 Contact: Robert Strausberg, Ph.D.
 Unpublished
Contact: Robert Strausberg, Ph.D.
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BI157032
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Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 785)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence start: 4
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 Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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 Contact: Robert Strausberg, Ph.D.
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 CDNA Library Preparation: Life Technologies, Inc.
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 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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INH-MGC http://mgc.nci.nih.gov/.
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COMMENT
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Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (199)."
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 Sequence 11, Application US/09854356
Patent No. US20020177567A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Dirk
APPLICANT: Coriax Corporation
APPLICANT: Coriax Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR PILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 111
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR PILILIGATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
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 APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/new Fusion Proteins
FILE REFRENCE: 014058-009810PC
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FRIOR FILING DATE: 1999-01-29
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 RESULT 3
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Publication No. US20030157113A1
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TILLE REPERENCE: 751708
CURRENT PAPLICATION NUMBER: US/09/751,708A
CURRENT PAPLICATION NUMBER: US/09/751,708A
CURRENT PAPLICATION NUMBER: US 60/173,371
PRIOR PAPLICATION NUMBER: US 60/173,371
 NAME/KEY: CDS
LOCATION: (26)...(3799)
LOCATION: (26)...(3799)
LOCATION: (26)...(1990)
NAME/KEY: misc_feature
LOCATION: (26)...(1990)
NAME/KEY: misc_feature
LOCATION: (2057)...(3796)
LOCATION: (2057)...(3796)
NAME/KEY: misc_feature
LOCATION: (2188)...(3022)
COTHER INFORMATION: kinase domain (KD) of rat HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2189)...(3022)
OTHER INFORMATION: kinase domain (KD) of rat HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2999)...(3796)
OTHER INFORMATION: phosphorylation domain (PD) of rat HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2999)...(3736)
 LOCATION: (2999)..(3173)
OTHER INFORMATION: preferred portion of the phosphorylation domain OTHER INFORMATION: (delta PD) of rat HER-2/neu
 3955
16
0
2
0
0
 3955
16
0
2
0
0
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-854-356-10 (1-3955)
 Matches:
Conservative:
Mismatches:
Indels:
 Matches:
Conservative:
Mismatches:
Indels:
 Length:
 Length:
 Gaps:
 OTHER INFORMATION: rat HER-2/neu cDNA
 NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
 0.00403
84.00
88.89%
88.89%
52.17%
TYPE: DNA
ORGANISM: Rattus norvegicus
 ORGANISM: Rattus norvegicus
 0.00403
 84.00
88.898
88.898
52.178
 ; LOCATION: (17)..(3799)
; OTHER INFORMATION:
US-09-751-708A-117
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
Best Local Similarity:
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Sequence 6, Application US/09930125

Publication No. US2002019332941

GENERAL INPORMATION:
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Edy, Teresa M.
APPLICANT: APPLICANT: Alos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
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APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APP
 APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Poy, Teresa M.
APPLICANT: Monell J.
APPLICANT: Monell, Patricia D.
APPLICANT: Monell, Patricia D.
APPLICANT: Wowlick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121:544 US/09/930,125
CURRENT APPLICATION NUMBER: US/09/930,125
 1713
14
2
2
0
0
 1755
14
2
2
0
0
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-10-378-393-14 (1-1713)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-930-125-6 (1-1755)
 Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 Matches:
 Matches:
 Length:
 Indels:
 Gaps:
 ; Sequence 4, Application US/09930125; Publication No. US20020193329A1; GENERAL INFORMATION:
 78.00
88.89%
77.78%
48.45%
 0.014
78.00
88.89%
77.78%
48.45%
 0.0136
 TYPE: DNA
ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens US-10-378-393-14
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 LENGTH: 1755
 Alignment Scores:
 US-09-930-125-6
 US-09-930-125-6
 US-09-930-125-4
 SEQ ID NO 6
 Query Match:
 No.:
 Pred. No.:
 Score:
 Score:
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 Sequence 14, Application US/10378393
Publication No. US20030182668A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
GENERAL GEN
 2990 GIGGTCATCCAGAACGAGGACTTGGGCCCATCCAGCCCCATGGACATACCTTC 3043
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 Sequence 165, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA13371C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 165
LENGTH: 1115
JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-751-708A-117 (1-3955)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-10-102-806-165 (1-1115)
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Gaps:
 NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 1713
TYPE: DNA
 0.0085
78.00
88.89%
77.78%
 ORGANISM: Homo sapiens
FEATURE:
 Percent Similarity:
Best Local Similarity:
Query Match:
 RESULT 5
US-10-102-806-165
 Alignment Scores:
 RESULT 6
US-10-378-393-14
 TYPE: DNA
 Pred. No.:
 ò
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```

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; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
 Query Match:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similari
 Alignment Scores:
 Alignment Scores:
 LENGTH: 1806
 RESULT 11
US-10-378-393-10
 US-10-207-498-5
 TYPE: DNA
 Pred. No.:
 RESULT 12
 ŏ
 Sequence 7, Application US/09930125

Publication No. US20020193329A1

GENERAL INFORMATION:

APPLICANT: Hand-Zimmerman, Susan

APPLICANT: Cheever, Martin A.

APPLICANT: Foy, Teresa M.

APPLICANT: Kalos, Michael J.

APPLICANT: More 1 D.

APPLICANT: More 1 D.

APPLICANT: Composition of HER-2/NEU-ASSOCIATED MALIGNANCIES

TITLE OF INVENTION: COMPOSITIONS AND METHOOS FOR THE THERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES

TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES

TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES

TITLE OF SEGURENT APPLICATION NUMBER: US/09/930,125

CURRENT APPLICATION NUMBER: US/09/930,125

CURRENT FILING DATE: 2001-08-14

NUMBER OF SEG ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 3.0

SEGUID NOS: 25

TENENT 1177
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 1773
14
2
2
0
0
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-930-125-4 (1-1767)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-930-125-7 (1-1773)
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Matches:
Conservative:
 Conservative:
Mismatches:
Indels:
 Mismatches:
Indels:
 Length:
Matches:
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1767
 Gaps:
 Sequence 5. Application US/09930125; Publication No. US20020193329A1 GENERAL INFORMATION:
APPLICANT: Hand-Zimmerman, Susan; APPLICANT: Cheever, Martin A. APPLICANT: Lodes, Michael J. APPLICANT: Kalos, Michael D.; APPLICANT: Moneill, Patricia D.; APPLICANT: Woweill, Patricia D.; APPLICANT: Vedvick, Thomas S.
 78.00
88.89%
77.78%
48.45%
 78.00
88.89%
77.78%
48.45%
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-930-125-4
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Alignment Scores:
 LENGTH: 1773
 RESULT 9
US-09-930-125-7
 US-09-930-125-5
 Query Match:
 Pred. No.:
 Pred. No.:
 Score:
 Score:
 ŏ
 δλ
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```
Sequence 10, Application US/10378393

Publication No US20030182668A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Carboni, Joan M.
APPLICANT: ROWLey, Ronald B.
APPLICANT: Wong, Tai W.
APPLICANT: Wong, Tai W.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVAT

TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
TITLE REFERENCE: D0224 NP
CURRENT APPLICATION NUMBER: US/10/378,393

CURRENT FILING DATE: 2003-03-03

PRIOR FILING DATE: 2002-03-03
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: .OF HER-2/NEU-ASSOCIATED MALIGNANCIES FILE REFERENCE: 210121.54 CURRENT APPLICATION NUMBER: US/09/930,125 CURRENT FILING DATE: 2001-08-14 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0
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22
20
0
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-10-378-393-10 (1-2411)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-930-125-5 (1-1806)
 Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 Length:
Matches:
 Matches:
 Length:
 Indels:
 ; Sequence 5, Application US/10207498
; Publication No. US20030143568al
; GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 2411
 78.00
88.89%
77.78%
48.45%
10
 78.00
88.89%
77.78%
48.45%
12
 0.0198
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-930-125-5
 ORGANISM: Homo sapiens US-10-378-393-10
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NAME/KEY: misc_feature
LOCATION: (1).(1959)
OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2026)..(3765)
OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2968)..(3765)
OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
 Sequence 2, Application US/09811115
Fatent No. US20020033736A1
GENERAL INFORMATION:
APPLICANT: Erickson, Sharon
APPLICANT: King, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENERY.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
SEQ ID NOS: 4
SEQ ID NOS: 4
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-811-115-2 (1-3768)
 GENERAL INCOMENTION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Dirk
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/nou Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT FAPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 69/493,480
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
 NAME/KEY: CDS
LOCATION: (1)..(3768)
OTHER INFORMATION: human HER-2/neu protein
 Sequence 9, Application US/09854356 Patent No. US20020177567A1
 78.00
88.89%
77.78%
48.45%
 TYPE: DNA
ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 ORGANISM: Homo sapiens
 Best Local Similarity:
 Percent Similarity:
 Alignment Scores:
 3768
 LENGTH: 3768
 US-09-811-115-2
 US-09-811-115-2
 US-09-854-356-9
 SEQ ID NO 9
 Query Match:
 FEATURE
 q
APPLICANT: Dennis J. Slamon
APPLICANT: Devid Elsenberg
TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HERECULIN AND MODULATING INTERACTIONS BETWEEN HERECULIN AND HER3
FILE REFERENCE: 30448.103-US-U1
CURRENT APPLICATION NUMBER: US/10/207,498
PRIOR APPLICATION NUMBER: 00/308,431
PRIOR APPLICATION NUMBER: 60/308,431
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LEWCTH: 3765
 Sequence 8, Application US/09811123
Fatent No. US2002001587A1
GENERAL INCORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
FILE OF INVENTION: MATHODY-MAYTANSINOID CONJUGATES
TITLE OF INVENTION: MATHODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENERY: 073A2
CURRENT FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-05
PRIOR PRIOR PLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 3768
TYPE: DNA
ORGANISM: Homo sapiens
US-09-811-123-8
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-10-207-498-5 (1-3765)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-811-123-8 (1-3768)
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Matches:
Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 0.0323
78.00
88.89%
77.78%
 78.00
88.89%
77.78%
48.45%
 0.0323
 TYPE: DNA
ORGANISM: Homo sapiens
 ; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 Alignment Scores:
Pred. No.:
 US-09-811-123-8
 Preď. No.:
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Length: Matches: Conservative: Mismatches:

Indels:

Gaps:

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; LOCATION: (2968)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (delta PD) of human HER-2/neu
US-09-854-356-9
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|------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|---------------------------------------------------------|
| го) от пишал нък-г/пец                                                 | Length: Matches: Conservative: Mismatches: Indels: Gaps:                                    | JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-854-356-9 (1-3768) |
| (מפדרמ                                                                 | 0.0323<br>78.00<br>88.89%<br>77.78%<br>48.45%                                               | (1-30) x                                                |
| , Olnen information: (deita PD) of indian BER-Z/Heu<br>US-09-854-356-9 | Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: | JUNC_SEQ8_SEQ2RES991_                                   |
|                                                                        |                                                                                             |                                                         |

Search completed: October 17, 2003, 03:53:07 Job time : 35.0111 secs

Qy Db

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Sequence 2, Appli
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Sequence 3, Appli
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 Sequence 1, A Sequence 1, A Sequence 5, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 3, A Sequence 4, A Sequence 4, A Sequence 3, A Sequence 3, A Sequence 3, A Sequence 3, A Sequence 4, A Sequence 3, A Se
 Sequence 10,
Sequence 25,
Sequence 27,
 Sequence 23
 Sequence
 Sequence 14, Application US/08229515A
Patent No. 5318885
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: BERB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
 COUNTRY
ZIP: 30303
ZIP: 30303
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994

***CONTRACTOR OF THE STATEMENT OF THE ST
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US-08-282-197C-1
US-09-252-991A-9985
US-09-214-808-1
US-09-214-808-1
US-09-252-991A-15154
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US-08-776-251-3
US-08-776-251-10
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US-09-547-435-29
US-09-547-435-29
US-09-25-388-5
US-09-925-388-5
US-09-229-3014-1
US-09-229-318-1
 US-09-103-840A-2
US-09-103-840A-1
 CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REPERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
 33,438
 TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THRRADS=1 - XGRPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 26, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 11, Appli
 (without alignments)
1741.185 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 October 15, 2003, 22:55:19 ; Search time 7.60488 Seconds
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/RE_TUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Re_TUS_COMB.seq:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame_plus_p2n model

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 US-08-625-101-1

US-08-135-786-1

US-09-048-804-1

US-09-056-105-26

US-08-645-865-9

US-08-645-865-9

US-09-167-322-4
 Total number of hits satisfying chosen parameters:
 US-08-229-515A-14
US-08-645-865-14
 US-09-527-487-1
US-09-877-177A-11
US-09-146-283-3
 569978 segs, 220691566 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
 JUNC_SEQ8_SEQ2RES991_
161
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 3955
3368
3768
3768
4473
4473
44530
4530
4530
2385
 Length
 Query
Match
 Title:
Perfect score:
Sequence:
 Scoring table:
 Score
 OM protein
 Searched:
 Run on:
 Result
 Š.
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Percent Similarity:
 ADDRESSEE:
 LOCATION:
 Alignment Scores:
 us-08-625-101-1
 US-08-625-101-1
 LENGTH:
 US-08-356-786-1
 qq
 2990 GTGGTCATCCAGAACGAGGACTTGGGCCCATCCAGCCCCATGGACAGTACCTTC 3043
 2990 GTGGTCATCCAGAACGAGGACTTGGGCCCCATCCAGCCCCATGGACAGTACCTTC 3043
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 APPLICANT: SARKAR, FAZLUL H
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
 3955
16
0
2
0
0
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-229-515A-14 (1-3955)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-645-865-14 (1-3955)
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATILLE
OPERATE: PASTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 Conservative:
Mismatches:
Indels:
 Conservative:
 Mismatches:
 ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
 Length:
Matches:
 Length:
Matches:
 Indels:
 ATTORNEY AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
RECISTRATION NUMBER: 33,438
REFERNCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-0770
TELEPHONE: 404-688-9880
 SOFTWARE: Patenta. SOFTWARE: PATENTAN DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
 Sequence 14, Application US/08645865
Patent No. 5654406
 TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
 3955 base pairs
 84.00
88.89%
88.89%
52.17%
 84.00
88.89%
88.89%
52.17%
STRANDEDNESS: single
 TYPE: nucleic acid STRANDEDNESS: single
 ZIP: 30303
COMPUTER READABLE FORM:
 ; TOPOLOGY: linear
US-08-229-515A-14
 linear
 GENERAL INFORMATION:
 Percent Similarity:
Best Local Similarity:
 Georgia
 Best Local Similarity:
 CITY: Atlanta
STATE: Georgia
 usa
 Percent Similarity:
 Alignment Scores:
 Alignment Scores:
 US-08-645-865-14
 US-08-645-865-14
 COUNTRY:
 LENGTH:
 Query Match:
 Query Match:
 Pred. No.:
 Score:
 ö
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COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE REACTIVITY TO HER-Z/Neu PROPEIN FOR PREVENTION OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-Z/Neu ONCOGENE IS ASSOCIATED
 2959 GIGGICAICCAGAAIGAGGACTIGGGCCCAGCCAGICCCTIGGACAGCACCTIC 3012
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe
 APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Oppermann, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Protein for Cancer
NUMBER OF SEQUENCES: 16
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-625-101-1 (1-3768)
 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
 Conservative:
Mismatches:
 ATORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 Matches:
 Indels:
 APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
Sequence 1, Application US/08625101
Patent No. 5869445
GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A. APPLICANT: Diss, Mary L. TITLE OF INVENTION: COMPOUNDS FRITLE OF INVENTION: OR TREATMENTITLE OF INVENTION: OR TREATMENTITLE OF INVENTION: ONCOGENE IS NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
 Sequence 1, Application US/08356786 Patent No. 5877305 GENERAL INFORMATION:
 3768 base pairs
 78.00
88.89%
77.78%
48.45%
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 Washington
 Best Local Similarity:
Query Match:
 STREET: 6300 CO
CITY: Seattle
STATE: Washingt
COUNTRY: USA
 NAME/KEY: CDS
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```
Sequence 26, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR;
TITLE OF INVENTION: PACCINES WITH ENHANCED INTRACELLULAR;
TITLE OF INVENTION: PACCINES WITH ENHANCED INTRACELLULAR;
TITLE OF INVENTION: WORDING: 23/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
NOFTWARE: FASTSEQ for Windows Version 3.0
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-056-105-26 (1-4473)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-048-804-1 (1-4473)
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 Length:
Matches:
Conservative:
Mismatches:
 Length:
Matches:
Conservative:
Mismatches:
 Indels:
 [ndels:
 CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGIGSTRATTON NUMBER: 38.534
REFERENCE/DOCKET NUMBER: ISIS-2913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4473 base pairs
TYPE: Nucleic Acid
cTRAEL ACID
 омВЕR: US/09/048,804
Herewith
 78.00
88.89%
77.78%
48.45%
 88.898
77.78
48.45
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: Herewith
CLASSIFICATION:
 TYPE: DNA ORGANISM: Homo sapiens
 STRANDEDNESS: Sing
TOPOLOGY: Unknown
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Alignment Scores:
 ANTI-SENSE:
 RESULT 6
US-09-056-105-26
 SEQ ID NO 26
LENGTH: 4473
 US-09-056-105-26
 US-08-229-515A-9
 US-09-048-804-1
 Query Match:
 Query Match:
 Pred. No.:
 qq
 US-09-048-804-1
| Sequence 1, Application US/09048804
| Sequence 1, Application US/09048804
| Patent No. 5968748
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
| TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
| TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
| STREET: One Liberty Place - 46th Floor
| COUNTRY: U.S.A.
| COUNTRY: U.S.A.
| COUNTRY: L.S.A.
 2959 GTGGTCATCCAGAATGAGGACTTGGGCCCAGCCCATCCCTTGGACAGCACCTTC 3012
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 3: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
Exchange Place, 53 State Street
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-356-786-1 (1-3768)
 LOCATION: 1..3768
OTHER INFORMATION: /note= "product = "cerB-b2""
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/831,967

FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: 27,829

REFERENCE/DOCKET NUMBER: 07000

TELEPHONE: (617) 248-7000

TELEPHONE: (617) 248-7100

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3768 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single
 CRP-053
 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 0.0285
78.00
88.89%
77.78%
CORRESPONDENCE ADDRESS:
 Massachusetts
 MOLECULE TYPE: CDNA
 linear
 Percent Similarity:
Best Local Similarity:
 NAME/KEY: CDS
 USA
 Boston
 02109
 Alignment Scores:
 Query Match:
 Pred. No.:
 à
```

```
SEQUENCE CHARACTERISTICS
 TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
 NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
 INFORMATION FOR SEQ ID NO:
 nucleic acid
EDNESS: single
 linear
 STATE: PA
 Percent Similarity:
Best Local Similarity:
 STRANDEDNESS:
 Alignment Scores:
 US-08-645-865-9
 US-09-167-322-4
 Query Match:
 δλ
 3109 GIGGICAICCAGAAIGAGGACIIGGGCCCAGCCAGCCCTIGGACAGCACCIIC 3162
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
APPLICANT: SARKAR, FAZUL H
APPLICANT: SARKAR, FAZUL H
TITLE OF INVENTION: BERB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
 APPLICAWT: RAZIUDDIN
APPLICAWT: SARKAR, FALUL H
APPLICAMT: SARKAR, FALUL H
TITLE OF INVENTION: ERBE2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-229-515A-9 (1-4530)
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 ATTORNEY/AGENT INFO 43-0

NAME: PERRYMAN, DAVID G

REGISTATION NUMBER: 33,438

REFERRNCE/DOCKET NUMBER: 1414.608

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-688-980

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 APPLICATION NUMBER: US/08/229,515A FILING DATE: 19 APR 1994 CLASSIFICATION: 435
 PC-DOS/MS-DOS
Sequence 9, Application US/08229515A Patent No. 5518885 GENERAL INFORMATION:
 US-08-645-865-9; Sequence 9, Application US/08645865; Patent No. 5654406
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 4530 base pairs
 0.036
78.00
88.89%
77.78%
 nucleic acid
EDNESS: single
 linear
 CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
 CITY: Atlanta
STATE: Georgia
COUNTRY: usa
 Percent Similarity:
Best Local Similarity:
 STRANDEDNESS:
 Alignment Scores:
 Query Match:
 RESULT 8
 Score:
 Pred.
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFCATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFERMATION:
 ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Suite 1800, Two Penn Center Plaza CITY: Philadelphia
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-645-865-9 (1-4530)
SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645 ace
 APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M. England, James M. TITLE OF INVENTION: CANCER VACCINE
 Conservative:
Mismatches:
 NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
 Matches:
 Length:
 Indels:
 APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1141.608
TELECOMMUNICATION:
TELEPHONE: 404-688-0770
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
 COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 Sequence 4, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
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Conservative: Mismatches:

0.036 78.00 88.89% 77.78%

Indels:

Matches:

Length:

S

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JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-877-177A-11 (1-4530)
 ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 US-09-877-177A-11
 Query Match:
 ..
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 Pred.
 q
 Sequence 11, Application US/09877177A

Sequence 11, Application US/09877177A

Patent No. 6582919

GENERAL INFORMATION:
APPLICANT: K. Danenberg

TITLE OF INVENTION: Method of determining Epidermal Growth
TITLE OF INVENTION: Aethod of determining Epidermal Growth
TITLE OF INVENTION: Method of Correlation of Levels Thereof With Survival
FILE REFERENCE: 11220/120

CURRENT APPLICATION UNMER: US/09/877,177A

CURRENT FILING DATE: 2001-06-11

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 4530
 1109 GIGGECATCCAGAATGAGGACTTGGGCCCAGCCAGCCCTTGGACAGCACCTTC 3162
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-167-322-4 (1-4530)
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-527-487-1 (1-4530)
 Length:
Matches:
Conservative:
Mismatches:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 APPLICANT: Nicolette, Charles
TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 4530
 Gaps:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 Gaps:
 Sequence 1, Application US/09527487 Patent No. 6528060 GENERAL INFORMATION:
 0.036
78.00
88.89%
77.78%
 0.036
78.00
88.89%
77.78%
 ; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 US-09-877-177A-11
 Alignment Scores:
 Alignment Scores:
 US-09-167-322-4
 US-09-527-487-1
 TYPE: DNA
 Query Match:
DB:
 Query Match:
 Pred. No.:
 Pred. No.:
 RESULT 10
 Score:
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2385
15
5
7
1
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
 US-09-146-283-3
Sequence 3, Application US/09146283
Sequence 3, Application US/09146283
Sequence 3, Application US/09146283
Sequence 3, Application US/09146283
Septicant No. 5996546
APPLICANT: Laus, Reiner APPLICANT: Ruegg, Curtis L. APPLICANT: Wu, Hongyu TITLE OF INVERTION: Immunostimulatory Compositions NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-146-283-3 (1-2385)
 Conservative:
Mismatches:
 Matches:
 Length:
 Indels:
 ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
REFERENCE/COCKET NUMBER: 7636-0010.21
TELECOMMUTCATION:
TELEPHONE: 650-324-0860
TELEPAX: 650-324-0960
 E: Dehlinger & Associates
350 Cambridge Ave. Suite 250
 TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
 0.556
68.00
68.97%
51.72%
42.24%
 STREET: 350 Cambi
CITY: Palo Alto
STATE: CA
COUNTRY: USA
 linear
 Percent Similarity:
Best Local Similarity:
 ORIGINAL SOURCE:
ORGANISM: hom
 Ş
 94306
 ADDRESSEE:
 Alignment Scores:
 ANTI-SENSE:
 US-09-146-283-3
```

```
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-09-344-195-3 (1-2385)
 Conservative:
Mismatches:
 REFERENCE/DOCKET NUMBER: 7636-0010.21
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24 Jun-1999
CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03.5EPT-1998
ATTORNEY/AGENT INFORMATION:
 1979 CCCGCCGCTCGCCCAGCCCCAGCACA 2005
 Length:
 Indels:
 21 GlyProSerSerProMetAspSerThr 29
 NAME: Judge, Linda R. REGISTRATION NUMBER: 42,702
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
 MEDIUM TYPE: Floppy disk
 Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL INFORMATION:
 RESULT 15
US-08-776-251-3
; Sequence 3, Application US/08776251
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 APPLICANT: Laus, Reiner
Ruegg, Curtis L.
 TYPE: nucleic acid
STRANDEDNESS: double
 SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pa
 ZIP: 94306
COMPUTER READABLE FORM:
 68.00
68.97%
51.72%
42.24%
 INFORMATION FOR SEQ ID NO:
 USA
 HYPOTHETICAL: NO ANTI-SENSE: NO
 ORIGINAL SOURCE:
 STATE: CA
COUNTRY: U
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 US-09-344-195-3
 US-09-344-195-3
 Pred
 g
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 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
ITITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
 DRGANISM: homo sapiens INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-579-823A-3 (1-2385)
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
 1979 CCCGCCGCTCGCCCAGCCCCAGCACA 2005
 Indels:
 1979 CCGCCCGCTCGCCCAGCCCCAGCACA 2005
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
 21 GlyProSerSerProMetAspSerThr 29
 21 GlyProSerSerProMetAspSerThr 29
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
 7636-0010
 Sequence 3, Application US/08579823A Patent No. 6080409 GENERAL INFORMATION:
 ATTORNEY AGENT INFORMATION:
NAME: Judge, Linda R.
REGIETRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
 MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid
 650-324-0960
 double
 linear
 Palo Alto
 INFORMATION:
 Percent Similarity:
Best Local Similarity:
 ANTI-SENSE: NO
ORIGINAL SOURCE:
 USA
 STRANDEDNESS:
 HYPOTHETICAL:
 94306
 ORGANISM:
 Alignment Scores:
 US-08-579-823A-3
 US-08-579-823A-3
 TELEFAX:
 COUNTRY:
 Query Match:
 RESULT 13
 qq
 ò
 δ
 q
 οy
```

```
Patent No. 6025340

GENERAL INVORMATION:
MARTALS RICHARD
MARTALS RICHARD
TITLE OF INVEWTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6023340th Glebe Road, 8th Floor
CITY:
ALIJINGTON:
STREET: 1100 No. 6023340th Glebe Road, 8th Floor
CITY:
ALIJINGTON:
COMPUTER READALE FORM:
WEDIUM TYPE: PLOPEY NESS:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ALIJINGTON NUMBER: US/G/MS-DOS
SOFTWARE: VIXALIAN-1997
SOFTWARE: PLOPEY NUMBER: US/G/MS-DOS
SOFTWARE: PLOPEY NUMBER: US/G/MS-DOS
SOFTWARE: PLOPEY NUMBER: US/G/MS-DOS
SOFTWARE: PLOPEY NUMBER: GB 9415167.7
FILING DATE: 27-JUL-1995
RECIPERATING DATA:
REPLICATION NUMBER: GB 9415167.7
FILING DATE: AT-LINGTON NUMBER: GB 9415167.7
FILING DATE: TROUGHTON NUMBER: CB 9415167.7
FILING DATE: AT-LINGTON NUMBER: CB 9415167.7
FILINGTON NUMBER: CB 9415167.7
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x US-08-776-251-3 (1-153)
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66.00
100.00%
78.57%
40.99%
 MOLECULE TYPE: CDNA
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 US-08-776-251-3
 Score:
 ò
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Search completed: October 16, 2003, 17:16:27 Job time : 16.6049 secs THIS PAGE BLANK (USPTO)

```
Human breast and o
Human cDNA for the
Human cDNA for the
Human cDNA for the
Human cDNA for the
Human HER-2/neu co
CDNA encoding huma
HER-2/neu oncogene
 Human HER-2 cDNA.
Human Her2 antigen
Human ERBB2 DNA SE
Human Her-2/neu pr
Human Her-2/neu cD
Human Her-2/neu cD
Human Polynucleoti
 Human HER-2/neu on
Human heregulin 2
Human HER-2/neu pr
Human ERBB2 polynu
 Human tumour antig
HER-2 nucleic acid
Human gene express
Human Her-2 DNA.
 Her-2/neu (ERBB2/c
Human HER2 gene.
 Nucleotide sequenc
Mouse Her-2/neu cD
 Rat neu promoter.
Rat HER-2/neu prot
 DNA fr
 Human HER2-neu SEQ
 Breast cancer asso
Human Her2/Neu enc
 Mouse Her-2/neu cD
 Nucleotide sequenc
 Human tyrosine kin
 Human gene express
 HER2 transgene pla
 Mouse Her-2/neu ex
 Human polynucleoti
Human HER2 (ErbB2)
 Her-2/neu extracel
 Sequence encoding cDNA encoding the
 Breast carcinoma
 Human ERBB2
 Mouse Her-2/neu extracellular-phosphorylation domain fusion cDNA.
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; mouse; gene therapy; gene; ss.
and is derived by analysis of the total score distribution
 ALIGNMENTS
 SUMMARIES
 AAD43935
AAD43986
 AB083856
AAF24297
 AAA09455
AAH23392
 ABZ35744
ABX09987
 ABL91709
ABK14058
 ABV78168
 AA260815
 ABZ35012
 ABN85585
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 AAD19731
 Location/Qualifiers
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 ABA92252 standard; cDNA; 2763 BP
 17-JUN-2002 (first entry)
 %
Query
Match Length I
 1806
 3768
3768
3768
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3768
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3768
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 3771
3955
3955
1115
1755
1767
 4473
4473
4473
 Mus musculus
 Score
 Key
 ABA92252
 Result
 õ
 (without alignments)
2842.104 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
 October 15, 2003, 21:06:28; Search time 28.4941 Seconds
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 5105512
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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 161
1 ERGCPAEQRASPVTFQNEDLGPSSPMDSTF 30
 hits satisfying chosen parameters:
 2552756 seqs, 1349719017 residues
 Maximum Match 100%
Listing first 45 summaries
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7.0
7.0
 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
 JUNC_SEQ8_SEQ2RES991
 Geneseq_19Jun03:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 BLOSUM62
 of
 score:
 Scoring table:
 Total number
 Database :
 Title:
Perfect so
Sequence:
 Searched:
 Run on:
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```
Her-2/neu extracellular-phosphorylation domain-TcP0 fusion cDNA
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; TcP0; mouse; gene therapy; gene; ss.
 JUNC_SEQ8_SEQ2RES991_ (1-30) x ABA92253 (1-2781)
 17-JUN-2002 (first entry)
 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAM51151). The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of human cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu vaccines comprising the fusion proteins, viral vectors, and vaccines comprising the fusion proteins, the ECD of Her-2/neu is fused to a cancer in preferred fusion proteins, the ECD of Her-2/neu is fused to a mimune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by canned the fusion protein in the form of a vaccine, or by canned to the animal. The fusion protein, uncleic acid, and isolated concer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu in the fusion protein cancer in a patient. T cells that specifically react with a Her-2/neu in the fusion protein cancer in a patient.
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 order to inhibit the development of cancer in a patient.
 Sequence 2763 BP; 571 A; 855 C; 772 G; 565 T; 0 other;
 /product= "Her-2/neu ECD-PD fusion"
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x ABA92252 (1-2763)
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Disclosure; Fig 23; 141pp; English.
 ABA92253 standard; cDNA; 2781 BP
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507.
 58e-12
 153.00
96.678
96.678
95.038
 phosphorylation domain
 Cheever MA, Gheysen D;
 WPI; 2002-241743/29.
P-PSDB; AAM51152.
 (CORI-) CORIXA CORP
 Percent Similarity:
Best Local Similarity:
Query Match:
 WO200212341-A2
 Alignment Scores:
Pred. No.:
 14-FEB-2002
 ABA92253;
 RESULT 2
 ABA92253
 Score:
ò
 ò
```

```
Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain.
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (EDD) and the concers, including breast, ovarian, colon, lung and prostate cancers. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu overexpression correlates with a poor prognosis. In proferred fusion proteins, the ECD of Her-2/neu is fusion proteins, the ECD of Her-2/neu is fusion proteins, the ECD of Her-2/neu is fusion proteins, the ECD of Her-2/neu is fusion protein in the form of a vaccine, or by administering the fusion protein in the form of a vaccine, or by a conding the fusion protein in the form of a vaccine, or by conding the fusion proteins, nucleic acids and isolated encoding the fusion proteins, nucleic acids, and isolated content of the animal. The fusion proteins, nucleic acids, and isolated content in a patient. T cells that specifically react with a Her-2/neu cancer in a patient. T cells that specifically react with a Her-2/neu content of the c
 /product= "Her-2/neu ECD-PD-TcP0 fusion"
 order to inhibit the development of cancer in a patient.
 Sequence 2781 BP; 574 A; 859 C; 779 G; 569 T; 0 other;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 (CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Location/Qualifiers
1..2781
/*tag= a
 Disclosure; Fig 25; 141pp; English.
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153.00
96.67%
96.67%
95.03%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507

 Mus musculus.
 Unidentified.

 Cheever MA, Gheysen D;
 WPI; 2002-241743/29.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAM51153
 WO200212341-A2.
 Alignment Scores:
Chimeric
```

junc\_seq8\_seq2res991\_.rng

```
The present sequence encodes a murine neu polypeptide. It is a murine homologue of human Her-2/neu. Neu polypeptides and polynucleotides are useful for inhibiting the development of a cancer, preferably breast cancer in a patient. They are also useful for stimulating and/or expanding T cells specific for Her-2/neu. They are useful for detecting and treating Her-2/neu malignancies. Neu polypeptides are useful
 Novel isolated murine homolog of human Her-2/neu useful for inhibiting development of cancer, preferably breast cancer in a patient -
 2962 GTGGTCATCCAGAACGAGGCTTAGGCCCCTCCAGCCCCATGGACAGCACCTTC 3015
 Nucleotide sequence of a murine neu polypeptide from C57B16 mice.
 polypeptide; Her-2; cancer; breast cancer; T cell expansion;
 Sequence 3771 BP; 808 A; 1105 C; 1068 G; 790 T; 0 other;
 3771
16
0
2
0
0
 Conservative:
 Mismatches:
Indels:
 /*tag= a
/product= "neu polypeptide"
 Length:
Matches:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x AAH42210 (1-3771)
 Gaps:
 Location/Qualifiers
 Claim 4; Fig 1A-B; 53pp; English.
 BP,
 ABA92251 standard; cDNA; 3771 BP
 CDNA; 3771
 29-DEC-2000; 2000WO-US35648
 99US-0474382
 17-SEP-2001 (first entry)
 84.00
88.89%
88.89%
52.17%
 17-JUN-2002 (first entry)
 0.0342
 for producing vaccines.
 WPI; 2001-441718/47.
 (CORI-) CORIXA CORP
 AAH42210 standard;
 Percent Similarity:
Best Local Similarity:
Query Match:
 P-PSDB; AAG62860
 WO200148205-A2
 29-DEC-1999;
 Alignment Scores:
 05-JUL-2001
 Spies AG;
 AAH42210;
 2962
 ABA92251;
 vaccine;
 Mus sp.
 Nen
 Key
 Score:
 QQ
 X Z X E
 ò
 The present sequence encodes the mouse Her-2/neu protein. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor [EGFR]. It probably plays a part in cell growth and/or differentiation. The Her-2/neu gene is an oncogene. An Her-2/neu fusion protein comprising a domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the Her-2/neu protein. It may be used to treat or brevent cancer by eliciting or enhancing an immune response to the Her-2/neu protein. It may be used to treat an abreast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 1 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 Her-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; ss.
 Sequence 3771 BP; 808 A; 1105 C; 1068 G; 790 T; 0 other;
 3771
16
0
2
0
0
 Length:
Matches:
Conservative:
 Mismatches:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x AAA89737 (1-3771)
 Indels:
 Disclosure; Fig 19; 128pp; English.
 AAA89737 standard; cDNA; 3771
 99US-0117976.
 28-JAN-2000; 2000WO-US02164
 (SMIK) SMITHKLINE BEECHAM
 0.0342
84.00
88.89%
88.89%
52.17%
 (first entry)
 Cheever MA, Gheysen D;
 Mouse Her-2/neu cDNA
 WPI; 2000-505976/45.
P-PSDB; AAB21206.
 (CORI-) CORIXA CORP
 Best Local Similarity:
 prostate cancers
 these neoplasias
 WO200044899-A1.
```

29-JAN-1999;

03-AUG-2000

12-JAN-2001

Mouse;

Mus sp.

AAA89737;

AAA8973

Percent Similarity

Query Match:

Alignment Scores:

Pred.

junc\_seq8\_seq2res991\_.rng

2962 GIGGICATCCAGAACGAGGACTTAGGCCCCTCCAGCCCCAIGGACAGGACCTC 3015

ВР

(first entry)

21-APR-1996

AAT01590;

Rat neu promoter.

Rattus rattus,

409528485-A1

13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe

30

```
Her-2/neu; c-erbB-2; oncogene; Erb-B2 promoter; DNA binding protein; HPBF; Erb-B2 promoter binding protein; tumour enhancer factor; breast cancer diagnosis; prognosis; antisense oligonucleotide; retro virus vector; gene therapy vector; ss.
 New purified protein binding to the ERBB2 gene promoter - to induce cell proliferation, diagnostic of breast cancer, also related antibodies, nucleic acid, assays and methods for screening
 AAT01590 standard; DNA; 3955
 AAT01590
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 The present sequence is that of murine Her-2/neu oncogene cDNA.

The CDNA can be obtained by PCR amplification (see ABA92255-56)
from mouse brain RNA. The Her-2/neu oncogene encodes a p185
glycoprotein (see AAM51151). The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, or the tyrosine kinase family of receptor-like glycoproteins.

Its overexpression correlates with a poor prognosis in breast and covering an encoder seem of the tyrosine kinase family of receptor-like glycoproteins.

Its overexpression correlates with a poor prognosis in breast and proteins, nucleic acides encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells cenceding the fusion protein, and delivering the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. I cells that specifically react with a Her-2/neu fusion protein cance temove tunnour cells from a sample in protein to the inhibit that a semple in protein.
 Her-2/neu, oncogene, cancer; tumour; vaccine; tyrosine kinase; receptor; mouse; gene therapy; gene; ss.
 order to inhibit the development of cancer in a patient.
 Sequence 3771 BP; 808 A; 1105 C; 1068 G; 790 T; 0 other;
 SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 /product= "Her-2/neu"
 Location/Qualifiers
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/*tag= a
 Disclosure; Fig 19; 141pp; English.
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
 Cheever MA, Gheysen D;
 phosphorylation domain
Mouse Her-2/neu cDNA.
 WPI; 2002-241743/29.
P-PSDB; AAM51151.
 (CORI-) CORIXA CORP
 WO200212341-A2.
 Mus musculus
 14-FEB-2002.
```

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Sarkar FH;

Raziuddin F,

WPI; 1995-373800/48.

94US-0229515. 95WO-US04953.

19-APR-1994;

19-APR-1995;

26-OCT-1995.

Disclosure; Page 57-59; 69pp; English.

inhibitors.

```
The sequence represents one of the promoters of the rat neu gene;

a second rat neu gene promoter is in AA701589. These promoter are
compared with the human Erb-B2 promoters (AA701589-88) and the mouse
neu promoter (AA701591). The human Erb-B2 gene is one of the mouse
primary genes responsible for the transition of normal breast
epithelial cells towards carcinoma in situ and the subsequent
development of invasive and mateastatic cancer. The Erb-B2
promoter-binding protein, HPBF (see AAR77093-94), induces cell
division on binding to the promoter. In a method for greater
cuccess in early identification and treatment of breast cancer,
the initation step for Erb-B2 gene activity is identified. This
method involves determining the presence of HPBF (relative to its absence
in a normal control) indicates the presence of Gancer and a
decreased chance of long-term survival. Binding of HPBF to the
connecter can be inhibited using antisense oligons can be
 expressed from retro virus or other gene therapy vectors
 Sequence 3955 BP; 842 A; 1147 C; 1136 G; 830 T; 0 other;
 Conservative:
 Mismatches:
Indels:
 Length:
Matches:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x AAT01590 (1-3955)
 84.00
88.89%
88.89%
52.17%
 0.0362
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
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3771 16 0

Length: Matches: Conservative: Mismatches:

84.00 88.89% 88.89% 52.17%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Pred. No.:

Indels:

(1-30) x ABA92251 (1-3771)

JUNC\_SEQ8\_SEQ2RES991\_

2990 GTGGTCATCCAGAACGAGGACTTGGGCCCATCCAGCCCCATGGACAGTACCTTC 3043

13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30

S

```
JUNC_SEQ8_SEQ2RES991_ (1-30) x AAA89753 (1-3955)
 RESULT
 g
 member of the tyrosine Kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in call growth factor receptor (EGFR). It here?/neu gene is an oncogene, An HER-2/neu fusion protein comprising a HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a domain may be used to treat or prevent cancer by aliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat alignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; st cancer; prostate cancer; ovarian cancer; lung cancer; n cancer; ds.
 Sequence 3955 BP; 842 A; 1147 C; 1136 G; 830 T; 0 other;
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/transl_except= (pos:1544..1546,aa.Gly)
/transl_except= (pos:1547..1549,aa.Leu)
/transl_except= (pos:1550..1552,aa.Glu)
 3955
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2
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 /product= "HER-2/neu protein"
 Rat HER-2/neu protein nucleotide sequence.
 Location/Qualifiers
26..3799
 Disclosure; Fig 16; 128pp; English.
 BP
 AAA89753 standard; DNA; 3955
 28-JAN-2000; 2000WO-US02164
 99US-0117976
 SMIK) SMITHKLINE BEECHAM.
 (first entry)
 0.0362
84.00
88.89%
88.89%
52.17%
 Cheever MA, Gheysen D;
 /*tag=
 WPI; 2000-505976/45.
P-PSDB; AAB21199.
 (CORI-) CORIXA CORP
 prostate cancers
 breast cancer;
 WO200044899-A1
 colon cancer;
 29-JAN-1999;
 Alignment Scores:
 12-JAN-2001
 03-AUG-2000
 Rattus sp
 AAA89753;
 . No. .
 Key
 RESULT 7
 AAA89753
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Best Local Similarity:

Query Match: DB:

Percent Similarity:

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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention and characterisation of the DNA and protein sequences of the isolation and characterisation of the DNA and protein sequences of the numerion. The breast and ovarian cancer associated DNA, protein, agonist or artagonist sequences exhibit cytostatic; immunosuppressive; noctropic; neuroprotective; antivital; antiallersic; hepatotropic; antiinfiammatory; antillicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer,
 New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
 nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis,
 Human breast and ovarian cancer associated antigen gene SEQ ID 165.
 arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as
 ds,
 Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabates mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease;
 Sequence 1115 BP; 210 A; 336 C; 338 G; 222 T; 9 other;
 1115
 cerebral anoxia and epilepsy; and infectious diseases
 Length:
 Claim 1; Page 604; 1299pp; English.
AAF21778 standard; DNA; 1115
 (HUMA-) HUMAN GENOME SCI INC.
 08-MAR-2000; 2000WO-US05881.
 99US-0124270.
 27-MAR-2001 (first entry)
 0.0601
 WPI; 2000-611515/58.
P-PSDB; AAB58875.
 Rosen CA, Ruben SM,
 WO200055173-A1.
 Homo sapiens.
 12-MAR-1999;
 Alignment Scores:
Pred. No.:
 21-SEP-2000.
 AAF21778;
```

```
AAD32744;
 Homo
 Key
 Score:
 88888888
 ŏ
 The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-1844 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplace molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 /*tag= a
/product= "Human protein encoded by cDNA for the clone
HICD_native_coding_region"
 Her-2/Neu polypeptide composition useful for therapy, diagnosis of cancer, preferably breast cancer
 Kalos MD;
 /transl_except= (pos:1741..1752, aa:Leu-Glu)
/note= "CDS does not include stop codon"
 Lodes MJ,
 00527
 Human cDNA for the clone HICD_native_coding_region
Matches:
Conservative:
 Mismatches:
 (1-30) x AAF21778 (1-1115)
 Indels:
 FOY TM,
 Example 5; Page 118-119; 129pp; English.
 Location/Qualifiers
 AAD32746 standard; cDNA; 1755 BP
 Cheever MA,
 14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733
 (first entry)
78.00
88.89%
77.78%
48.45%
 /partial
 Vedvick TS;
 WPI; 2002-280758/32.
 (CORI-) CORIXA CORP.
 Hand-zimmermann S,
 Best Local Similarity:
 JUNC_SEQ8_SEQ2RES991_
 P-PSDB; AAE20483
 WO200214503-A2
 Novel isolated prevention and
 Percent Similarity:
 01-JUL-2002
 Homo sapiens
 Mcneill PD,
 21-FEB-2002
 AAD32746;
 446
 Query Match:
 RESULT 9
 g
```

```
The invention relates to an isolated Her-2/New polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of
polypeptide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cance preferably for the immunotherapy of breast cancer and other Her-Z/Neusasociated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_native_coding_region.
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss
 "Human protein encoded by cDNA for the clone
 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe
 Kalos MD;
 Sequence 1755 BP; 376 A; 517 C; 531 G; 331 T; 0 other;
 Lodes MJ,
 Human cDNA for the clone HICD_CT_His_coding_region.
 Matches:
Conservative:
 Mismatches:
 (1-30) x AAD32746 (1-1755)
 HICD_CT_His_coding_region"
 Length:
 Indels:
 Foy TM,
 Example 5; Page 117-118; 129pp; English.
 Location/Qualifiers
 BP
 Cheever MA,
 AAD32744 standard; cDNA; 1767
 14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733
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88.89%
77.78%
 (first entry)
 /*tag= a
 /product=
 Hand-zimmermann S, C
Mcneill PD, Vedvick
 WPI; 2002-280758/32.
P-PSDB; AAE20481.
 (CORI-) CORIXA CORP.
 Percent Similarity:
Best Local Similarity:
Query Match:
 JUNC_SEQ8_SEQ2RES991_
 WO200214503-A2
 Alignment Scores:
 sapiens
 01-JUL-2002
```

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human malignancies, for stimulating and/or expanding T cells specific for patient. The invention is useful for stimulating at cell response in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in proprietation to therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_CT_His_coding_region.
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 "Human protein encoded by cDNA for the clone
 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer \,
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 Kalos MD;
 Sequence 1767 BP; 381 A; 521 C; 529 G; 336 T; 0 other;
 Human cDNA for the clone HICD_in_pPDM_coding_sequence.
 Lodes MJ,
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 /product= "Human protein enco
HICD_in_pPDM_coding_sequence'
 JUNC_SEQ8_SEQ2RES991_ (1-30) x AAD32744 (1-1767)
 Foy TM,
 Gaps:
 ocation/Qualifiers
 Example 5; Page 119; 129pp; English
 AAD32747 standard; cDNA; 1773 BP
 Cheever MA,
 14-AUG-2001; 2001WO-US41733,
 14-AUG-2000; 2000US-225152P.
 28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
 0.105
78.00
88.89%
77.78%
48.45%
 (first entry)
 Ø
 Hand-zimmermann S, Chee
Mcneill PD, Vedvick TS;
 /*tag=
 (CORI-) CORIXA CORP.
 WPI; 2002-280758/32.
P-PSDB; AAE20484.
 Percent Similarity:
Best Local Similarity:
 WO200214503-A2
 Homo sapiens
 Alignment Scores:
Pred. No.:
 01-JUL-2002
 21-FEB-2002.
 AAD32747;
 Query Match:
 RESULT 11
 Key
 Score:
 88888888888888888
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of cance of thuman malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centure Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in preferably for the immunotherapy of breast cancer and other Her-2/Neu associated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_in_ppDM_coding.
 Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ss.
 /*tag= a
/product= "Human protein encoded by cDNA for the clone
HICD_plus_B_HIS"
/transl_except= (pos:1543..1545, aa:Pro)
 30
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe
 Kalos MD;
 Sequence 1773 BP; 383 A; 528 C; 530 G; 332 T; 0 other;
 Lodes MJ,
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 (1-30) x AAD32747 (1-1773)
 Human cDNA for the clone HICD_plus_8_HIS.
 Foy TM,
 Gaps:
 Location/Qualifiers
1..1803
 AAD32745 standard; cDNA; 1806 BP.
 Hand-zimmermann S, Cheever MA,
Mcneill PD, Vedvick TS;
 14-AUG-2000; 2000US-225152P. 28-SEP-2000; 2000US-236428P. 21-FEB-2001; 2001US-270520P.
 14-AUG-2001; 2001WO-US41733.
 0.105
78.00
88.89%
77.78%
 01-JUL-2002 (first entry)
 (CORI-) CORIXA CORP.
 Percent Similarity:
Best Local Similarity:
 JUNC_SEQ8_SEQ2RES991_
 WO200214503-A2
 Homo sapiens
 Alignment Scores:
 21-FEB-2002.
 AAD32745;
 sednence
 Query Match:
 RESULT 12
 Score:
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RESULT 14
 ABK86207
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 diffective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the latest where the patient is human leukoyte antigen (HLA)-844 positive or is affected with brasat cancer. The composition is useful for the therapy and diagnosis of cancer. The composition for the diagnosis, prevention and treatment of and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for her-2/Neu polypeptide and for inhibiting the development of cancer in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the numan patient a suitable library and to direct expression of a polypeptide in appropriate host cells. The composition is useful in length gene from a suitable library and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neurassociated malignancies. The invention is useful in gene therapy. The present sequence is human cDNA for the clone HICD_plus_HIS.
 invention relates to an isolated Her-2/Neu polypeptide composition
 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
 Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
breast cancer; prostate cancer; ovarian cancer; lung cancer;
colon cancer; ds.
 Sequence 1806 BP; 391 A; 530 C; 544 G; 341 T; 0 other;
 Matches:
Conservative:
Mismatches:
 /*tag= a
/product= "HER-2/neu protein"
 JUNC_SEQ8_SEQ2RES991_ (1-30) x AAD32745 (1-1806)
 Length:
 Indels:
 5; Page 118; 129pp; English
 Location/Qualifiers
1..3600
 Human HER-2/neu coding sequence.
 ВР
 AAA89736 standard; DNA; 3600
 28-JAN-2000; 2000WO-US02164
 99US-0117976
 (first entry)
 0.108
78.00
88.89%
77.78%
 WPI; 2002-280758/32.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAE20482
 WO200044899-A1
 Homo sapiens
 29-JAN-1999;
 Alignment Scores:
 L2-JAN-2001
 03-AUG-2000
 994
 AAA89736;
 Example
 Query Match:
 RESULT 13
 AAA8973
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cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepadmavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 The present sequence encodes the human HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovvarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 /product= "Breast cancer antigen Her2 variant"
 Sequence 3600 BP; 723 A; 1108 C; 1075 G; 694 T; 0 other;
 cDNA encoding human breast cancer antigen, Her2 variant.
 Human; Her2; cytostatic; antiviral; immunostimulant;
 Conservative:
Mismatches:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x AAA89736 (1-3600)
 Length:
Matches:
 Indels:
 Gaps:
 Location/Qualifiers
7..3678
/*tag= a
 Disclosure; Fig 15; 128pp; English.
 ABK86207 standard; cDNA; 3678 BP
 01-NOV-2000; 2000US-0704232.
 01-NOV-2001; 2001WO-US45626
(CORI-) CORIXA CORP. (SMIK) SMITHKLINE BEECHAM.
 P-PSDB; AAB21198, AAB21208
 0.248
78.00
88.89%
77.78%
 24-SEP-2002 (first entry)
 WPI; 2000-505976/45
 Similarity:
 prostate cancers
 these neoplasias
 WO200240059-A2
 Percent Similarity:
 Homo sapiens
 Alignment Scores:
 23-MAY-2002
 Cheever MA,
 ABK86207;
 Query Match:
 Best Local
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JUNC_SEQ8_SEQ2RES991_ (1-30) x AAT40739 (1-3768)
 Search completed: October 15, 2003, 23:48:45 Job time: 32.4941 secs
WO9630514-A1
 Score:
 The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example tumnour cells.

Creating a subject having undesired cells, for example tumnour cells, for usually infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynuclectide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and leukaemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lenturinuses (including human immunodeficiency virus (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present sequence represents the coding sequence of human breast cancer antigen, HerZ variant, used as a target cantigen in the method of the invention.
 by
of
 Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen a cell, comprises administering a polynucleotide encoding a variant an antigen
 /*tag- b
//note= "nucleotides 2026-3765 (claim 1) code for
HER-2/neu intracellular domain"
 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
 Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 JUNC_SEQ8_SEQ2RES991_ (1-30) x ABK86207 (1-3678)
 AMERICAN FOUND BIOLOGICAL RES INC. MINCHEFF M S. LOUKINOV D I.
 Disclosure; Page 128-134; 146pp; English.
 Gaps:
 Zoubak S;
 Location/Qualifiers
 AAT40739 standard; cDNA; 3768 BP
 Mincheff MS, Loukinov DI,
 0.254
78.00
88.89%
77.78%
 01-JAN-1997 (first entry)
 WPI; 2002-527524/56.
P-PSDB; AAU98923.
 HER-2/neu oncogene.
 Percent Similarity:
Best Local Similarity:
 (ZOUB/) ZOUBAK S.
 Homo sapiens.
 Alignment Scores:
 AAT40739;
 MINC/)
 LOUK/)
 Query Match:
 Score:
```

á

```
Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbb2) protein (AAW01111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Lys676-Val1255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral vector, for genetic immunisation of an animal.
 DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Claim 1; Page 49-56; 71pp; English.
 96WO-US01689
 95US-0414417
 0.262
78.00
88.89%
77.78%
 (UNIW) UNIV WASHINGTON
 Cheever MA, Disis ML;
 WPI; 1996-455361/45.
P-PSDB; AAW01111.
 Best Local Similarity:
 Percent Similarity:
28-MAR-1996;
 31-MAR-1995;
 Alignment Scores:
 Query Match:
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BC027080 Mus muscu
AX189662 Sequence
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AX384607 Sequence
AX384608 Sequence
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AX384610 Sequence
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I21124 Sequence 9
I59745 Sequence 9
MI1730 Human tyros
AX660703 Sequence
AF393158 Rattus no
 AX481438 Sequence
AB008451 Canis fam
AR080259 Sequence
AR167390 Sequence
 X03363 Human c-erb
AR202597 Sequence
AR283481 Sequence
AX282577 Sequence
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Sequence
 AC098491 Rattus no
AB096612 Homo sapi
 Sequence
 AX587649 Sequence
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 AX201817 S
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 ALIGNMENTS
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 HAMNEU
 HSERB2R
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Match Length
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52.2 4694
50.6 186134
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 13450
 em sy
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444444444444444444000
 444444444444
 Score
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12533
8844
884448
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 RESULT 1
 Result
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 5777422
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - nucleic search, using frame_plus_p2n model
 161
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 2888711 seqs, 20454813386 residues
 Total number of hits satisfying chosen parameters:
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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 Title:
Perfect score:
 Scoring table:
 Sequence:
 Searched:
 Database
 Run on:
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Mus musculus
 Contact: amg@bcm.tmc.edu
 GI:20071980
 1 (bases 1 to 2083)
 2 (bases 1 to 2083)
Strausberg, R.
Direct Submission
 Seguencing Center
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 12477932
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 AUTHORS
TITLE
 RESULT 3
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 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 JOURNAL
 PUBMED
 REFERENCE
 JOURNAL
 REMARK
COMMENT
 TITLE
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 PAT 18-MAR-2002
 PAT 18-MAR-2002
 Her-2/neu fusion proteins
Patent: WO 0212341-A 28 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualifiers
 S.A. (BE)
 GluArgGlyCysProAlaGluGlnArgAlaSerProValThrPheGlnAsnGluAspLeu 20
 Her-2/neu fusion proteins
Patent: WO 0212341-A 30 14 FEB-2002;
CORIXA CORPORATION (US) ; SMITHKLINE BEECHAM BIOLOGICALS
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 Cheever, M.A. and Gheysen, D.
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96.67%
95.03%
 synthetic construct
 synthetic construct
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AX380942
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Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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BCU27080 2083 bp mRNA linear ROD 16-APR-2003 Mus musculus v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian), mRNA (CDNA clone MGC:38648 IMAGE:5356166), complete cds.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://lmage.llnl.gov Series: IRAK Plate: 54 Row: c Column: 18 This clone was selected for full length sequencing because it
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capabs-refemail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CoMA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
 Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 human and mouse cDNA sequences
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PAT 18-MAR-2002
 PAT 18-MAR-2002
 Cheever, M.A. and Gheysen, D.
Her-2/neu fusion proteins
Patent: WO 0212341-A 11 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
 Cheever,M.A. and Gheysen,D.

Her-2/neu fusion proteins
Patent: WO 0212341-A 10 14-FEB-2002;
CORIXA CORPORATION (US) ; SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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88.89%
88.89%
52.17%
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 Percent Similarity:
Best Local Similarity:
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 ø
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 Mus sp.
Mus sp.
 Rattus.
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Pred. No.:
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Pred. No.:
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Bargmann, C.I., Hung, M.C. and Weinberg, R.A.
The neu oncogene encodes an epidermal growth factor receptor related protein
Nature 319 (6050), 226-230 (1986)
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 PAT 07-0CT-1997
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridde; Murinae;
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 glycoprotein; kinase; neu oncogene; oncogene; transmembrane protein; tyrosine kinase.
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Conservative:

Mismatches: Indels:

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Loffs,F.J., Hurst,H.C., Sternberg,M.J. and Gullick,W.J.
Specific short transmembrane sequences can inhibit transformation
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Generation and initial analysis of more than 15,000 full-length
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0
 ROD 22-APR-2003
 Thomas L. Casavant.
Web site: http://genome.ulowa.edu
Contact: bento-soares@ulowa.edu; tom-casavant@ulowa.edu
Bonaldo,WrF., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4694)
 Submitted (13-FEB-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 Mus musculus v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neurc/glioblastcma derived oncogene homolog 2, neurc/glioblastcma derived oncogene homolog (avian), mRNA (cDNA clone MGC:61178 IMAGE:5702040), complete cds. BC046811
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 13 ValThrPheGlnAsnGluAspLeuGlyProSerSerProMetAspSerThrPhe 30
 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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(1-30) x RNNEUR (1-3955)
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 Mus musculus (house mouse)
Mus musculus
 BC046811.1 GI:28386210
 (bases 1 to 4694)
 Direct Submission
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 REFERENCE
AUTHORS
 TITLE
JOURNAL
 PUBMED
 JOURNAL
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 COMMENT
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Diatchenko, L., Maruslna, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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1 (bases 1 to 4695)
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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Mus musculus cDNA clone MGC:62447 IMAGE:5702040, complete cds.
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0
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 RESULT 11
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Scheln, J.E., Jones, S.J. and Marra, M.A.,
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Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Meb site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
 TDTFESMLNPEGRYTFGASCVTTCPYNYLSTEVGSCTLVCPPNNQEVTAEDGTQRCEK
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 Direct Submission
Submitted (02-JUN-2003) National Institutes of Health, Mammalian
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Best Local Similarity:
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 1 (bases 1 to 4727)
Watson,P.A., Kim,K., Chen,K.-S. and Gould,M.N.
Androgen-Dependent Mammary Carcinogenesis in Rats Transgenic for
 Chen,K..S., Watson,P.A. and Gould,M.N.

Chen,K..S., Watson,P.A. and Gould,M.N.

Direct Submission
Submitted (29-MAY-2002) Oncology, University of Wisconsin, 1400
University Ave., Madison, WI 53706, USA
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Cambridgeshire, CBIO 15A, UK E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 200, 2001 this sequence version replaced q1:16555512.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was faintshed as follows unless otherwise noted: all
regions were either double-stranded or sequencing problems, such
chemistry or covered by high quality data (1.e., phred quality) -
30); an attempt was made to resolve all sequencing problems, such
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one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORNDEP; Information on the WORNDEP
 IMPORTANT: This sequence is not the entire insert of clone RP23-355110 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP23-355110 is at 186134 in this sequence. The true right end of clone RP23-35510 is at 186134 in this
 ROD 17-NOV-2001
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Phillimore, B.
Direct Submission
 Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-355L10 is
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-16614
 Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 2, 2001 this sequence version replaced gi:12061538.
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Mus musculus chromosome 11 clone RP23-16G14 map 11, WORKING DRAFT
 Center: Whitehead Institute/ MIT Center for Genome Research
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mus musculus
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Sequencing vector: plasmid; mivible 304 of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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Insert size: 219719; sum-of-contigs
Quality coverage: 8.5 in Q20 bases; agarose-fp
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Quality coverage: 7.8 in Q20 bases; agarose-fp
Quality coverage: 7.8 in Q20 bases; are correctly
* NOTE: This is a "working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence reford is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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 COPONSTETCTGSEADOCTACPHYRDSPFCVARCPSGVRPDLSYMPIWKYPDEEGWCO
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 BASE COUNT
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 Score:
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 D16295.1 GI:493236
EGF-receptor; cellular oncogene; neu-differentiation
EGF-receptor; cellular oncogene; neu-differentiation
factor/berequlin; tyrosine kinase.
factor/berequs auratus (golden hamster)
Mesocricetus auratus
Besocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 Mesocricetus.

1 (bases 1 to 4062)
Nakamura,T., Ushijima,T., Ishizaka,Y., Nagao,M., Arai,M.,
Yamazaki,Y. and Ishikawa,T.
Cloning and activation of the Syrian hamster neu proto-oncogene 6ene 140 (2), 251-255 (1994)
 Direct Submission
Submitted (19-MAY-1993) Takuro Nakamura, Faculty of Medicine,
University of Tokyo, Department of Pathology; 7-3-1 Hongo,
Bunkyo-ku, Tokyo 113, Japan (Tel:81-3-3812-2111(ex.3356),
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Nakamura, T.
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VERSION
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JOURNAL
MEDLINE
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TITLE
JOURNAL
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 RESULT 15
 PUBMED
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LOCUS
 SOURCE
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ò g ò

Job time : 465.208 secs

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Mus musculus
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85
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 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
DEFINITION
 ACCESSION
 REFERENCE
 RESULT 1
AZ699313
 Result
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 ပ
 O
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 45562784
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

 nucleic search, using frame_plus_p2n model

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 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-RÇ3&t2-RC3-HT0371-S09100-013-e06&t3=2000-01-29&t4=1)
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High quality sequence start: 8
High quality sequence stop: 422.
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1 (bases I to 439)

1 (bases)

 316 ATGCTGGGCTGGGGAGGGGCCACCATCCTCCTTCCTCCACAGAATGAGGACTTG 375
 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 256 ccrecadadegregeaagaagargagrecadraargccaggcccreaceaaggcrec
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Best Local Similarity:
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 BASE COUNT
ORIGIN
 RESULT 3
BE157169/c
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9
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COMMENT
 DEFINITION
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VERSION
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SOURCE
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 REFERENCE
 AUTHORS
 FEATURES
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EcoRI sites. The ligation products were transformed into
BHIOB electrocompetent cells (BRL Life Technologies). "
214 c 151 g 143 t
 AW606421 EST 23-MAR-2000 RC3-HI0371-290100-013-e06 HT0371 Homo sapiens cDNA, mRNA sequence.
 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.oho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
 618
18
3
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20

| JOURNAL Unpublished COMMENT Contact: Daniels Office of Cancer National Cancer Bidg: 31 Rm10AO/ Email: cgapbs-r/ Email: cgapbs-r/ Tissue Procurem CONA Library PA                                                                                                                                                                         | DNA Sequencing Clone distribut Clone distribut found through the http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://image.lli http://im | /db_xre/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clone/clon | Alignment Scores: Pred. 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|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------|----------------------------|--------------------------------------------|-----------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------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| TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  MEDLINE 20202663  COMMENT 20202663  COMMENT Laboratory of Cancer Genetics  Ludwig Institute for Cancer Research  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | source 1. 439 /organism="Nomo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /dow_stage="Adult" /clone_lib="Hr0371" /note="Organ: head_neck; Vector: puc18; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products Gerlyed from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  BASE COUNT 89 a 139 c 132 g 79 t                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Alignment Scores: 0.262 Length: 439 Pred. 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REFERENCE 1 (bases 1 to 944) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) |

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458 bp mRNA linear EST 21-JUN-2000 200-015-h07 HT0371 Homo sapiens CDNA, mRNA sequence.
 Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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troopen). Note: this is a NIH_MGC_Library."
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 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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458)
 remail.nih.gov
mient: Dr. Michael Brownstein
Preparation: Invitrogen Corp
Arrayed by: The I.M.A.G.E. Consortium (LLNL)
up by: Agencourt Bioscience Corporation
bution: MGC clone distribution information can be
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PUBMED
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Email: asimpson@ludwig.org.br
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Project. This end be seen in the following URL
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 BF869854 117-JAN-2001 IL3-ET0114-251000-317-BF0 ET0114 Homo sapiens CDNA, mRNA sequence. BF869854
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.Y., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. Soares of the human transcriptome with ORF expressed
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 378)
 Shotgun sequencing of the human transcriptome with ORF expressed
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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81.00
88.89%
88.89%
50.94%
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 Percent Similarity:
Best Local Similarity:
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 Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 Fax: +55-II-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=II]3&t2=IL3-ET0114-
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Homo sapiens mRNA; EST DKF2p686K21213_r1 (from clone DKF2p686K21213)
 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
 237 GACAAGGGCTGCCCGCCGAGCAGCAGCCAGCCCTTTGACGTCC 193
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 378
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Last updated, Version 1)
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Location/Qualifiers
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 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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 Contact: Simpson A.J.G.
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100.00%
 Homo sapiens (human)
 rel: +55-11-2704922
 Fax: +55-11-2707001
 50.31%
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 Percent Similarity:
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 Best Local
 BASE COUNT
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9
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VERSION
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 AUTHORS
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 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ): Email s.wiemanneGkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project.
 No s1 sequence available.
This clone (DKFZp686K21213) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
 411
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 Contact: Simpson A.J.G.
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50.31%
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 rel: +55-11-2704922
 Fax: +55-11-2707001
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 Homo sapiens
 Simpson, A.J.
 Similarity:
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 Percent Similarity
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 Sequence 411
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 Best Local
 Pred. No.:
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VERSION
 REFERENCE
AUTHORS
 JOURNAL
MEDLINE
PUBMED
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 COMMENT
 SOURCE
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Score:

LOCUS

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 Email: benco-soares@ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 Reverse.
 Eukaryota.

Eukaryota.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 466),

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
 Tel: 319 335 8250
Fax: 319 335 8250
Eax: 319 335 9565
 Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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MEDLINE
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Matches:

Length:

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 7375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9250
Fax: 319 335 9555
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
 first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 561)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
 Jinear EST 01-01.E-E00-ahz-c-05-0-UI.rl UI-E-E00 Homo sapiens cDNA clone UI-E-E00-ahz-c-05-0-UI.s', mRNA sequence.
 Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242
 Genetics (www.resgen.com).
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Location/Qualifiers
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80.00
100.00%
100.00%
50.31%
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 Homo sapiens
 Percent Similarity:
Best Local Similarity:
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 JOURNAL
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 BM720098
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following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |" Life Technologies).
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie Wark EST Project 1997
 (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
 EST 03-JUN-1997
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AA443351 SOATES_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:783729 5' similar to gb:M11730 ERBB-2 RECEPTOR PROFEIN-TYROSINE KINASE PRECURSOR (HUMAN);, mRNA sequence.
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -26ml3 rev2 ET from Amersham
High quality sequence stop: 360.
Location/Qualifiers
 Double-stranded cDNA was ligated to Eco RI adaptors
 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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 AA443351.1 GI:2156026
 1.49
80.00
100.00%
100.00%
50.31%
 Homo sapiens (human)
 Homo sapiens
 Percent Similarity:
Best Local Similarity:
 Unpublished
 Alignment Scores:
 EST
 Query Match:
DB:
 DEFINITION
 BASE COUNT
ORIGIN
 Pred. No.:
 ORGANISM
 ACCESSION
VERSION
KEYWORDS
SOURCE
 TITLE
JOURNAL
COMMENT
 RESULT 12
 REFERENCE
 AUTHORS
 AA443351
 FEATURES
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 Mismatches:
Indels:
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Matches:
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 mRNA sequence.
AW410534
AW410534.1 GI:6936075
 Homo sapiens (human)
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100.00%
50.31%
 80.00
100.00%
100.00%
50.31%
 1.7
80.00
 Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 Query Match:
DB:
 source
 KEYWORDS
SOURCE
ORGANISM
 BASE COUNT
ORIGIN
 DEFINITION
 .. ON .
 ACCESSION
VERSION
 AUTHORS
TITLE
JOURNAL
COMMENT
 RESULT 15
 REFERENCE
 AW410534
 FEATURES
 Score:
 Score:
 ă
 AL Oppublished
Other ESTS: BEG1550
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore CA, USA
Livermore CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact information on obtaining this clone, please contact
Information on obtaining this clone, please contact
Information on obtaining this clone, please contact
Information on obtaining this clone, please contact
Information on obtaining this clone, please contact
Information on obtaining this clone, please contact
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Information on obtaining this clone, please contact
Information on obtaining this clone, please contact
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Information on obtaining this clone, please contact
Information on obtaining this clone, please contact
Information on obtaining this clone, please resistant)
Information of the laboratory of Gerald M. Rubin
Information of the laboratory of Gerald M. Rubin
Information of the laboratory of Gerald M. Rubin
Information of the laboratory of Gerald M. Springer, as synthesis kit (Stratagene) and Superscript II RT (Life
Information) Information of the laboratory of Information of I
 EST 16-NOV-2001
was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)." 171~c~179~g~113~t~1~others
 BMOB3444 16-NOV-200 16-NOV-200 mRNA linear EST 16-NOV-200 imageqc_6_2000/sjp459bdff42.x2 NIH_MGC_39 Homo sapiens cDNA clone mRAE:3610674 5', mRNA sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 607)
 Kale, P.I., Harsch, T.J., Folta, P.A., Nelson, D.O., Sanders, C.G. and Prange, C.K.
The I.M.A.G.E. Consortium quality control effort: clone resequencing for verification
 400 GACAAGGGCTGCCCCCCCCGCCGAGAGCCAGCCCTCTGACGTCC 444
 12
 2 others
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 561
0
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 121 t
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 195 g
 BM083444.1 GI:16951075
 Technologies)
 Homo sapiens (human)
 1.54
80.00
100.00%
100.00%
50.31%
 Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 ಡ
 ದ
 BM083444
 97
 Alignment Scores:
 EST
 ..
0
 DEFINITION
 BASE COUNT
ORIGIN
 BASE COUNT
 ORGANISM
 RESULT 14
BM083444
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
 ORIGIN
 Score:
 ŏ
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Tissue procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.AG.E. Consortium (LLNL)

Sequencing Center (NISC)

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/Aimage/Aimage html

Plate: LLCMG6 row: O column: 12

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 613)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
613
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0
0
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 JUNC_SEQ3_SEQ5 (1-30) x AW410534 (1-613)
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qq δ

Search completed: October 16, 2003, 17:04:03 Job time: 235.794 secs

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Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 12, Appli
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Sequence 12, Appli
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Sequence 132, Appli
Sequence 1332, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 2, Appli
 Sequence 3, Application US/10109213
Publication No. US20020168670A1
Publication No. US20020168670A1
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
FILE REFERENCE: IBISO009
CURRENT PAPLICATION NUMBER: US/10/109,213
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US/09/200,355
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12 US-10-207-498-5
9 US-09-811-123-8
9 US-09-811-115-2
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11 US-09-111-115-1
12 US-10-313-644-1
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Conservative:
Mismatches:
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 - nucleic search, using frame_plus_p2n model
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 1750203 seqs, 1313063994 residues
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Perfect score:
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 Result
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RESULT

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GENERAL INFORMATION:
APPLICANT: Erickson, Sharon
APPLICANT: Erickson, Sharon
APPLICANT: Schwall, Ralph
APPLICANT: Schwall, Ralph
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENERT. 034A
CURRENT APPLICATION NUMBER: 05/09/811,115
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
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Mismatches:
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Mismatches:
Indels:
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US-99-84-356-9
Sequence 9, Application US/09854356
Patent No. US2002017567A1
GENERAL INFORMATION:
APPLICANT: Gheever, Martin A.
APPLICANT: Gheever, Martin A.
TILE OF INVENTION: HER 2.7 new Fusion Proteins
FITLE OF INVENTION: HER 2.7 new Fusion Proteins
FILE OF INVENTION: HER 2.0 new Fusion Proteins
FILE OF INVENTION: HER 2.0 new Fusion Proteins
FILE OF INVENTION: HER 2.0 new Fusion Proteins
FILE OF INVENTION HERE: 0.9/99.954,356
CURRENT APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN OF 2.1
SEQ ID NO 9
LENGTH: 3768
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 JUNC_SEQ3_SEQ5 (1-30) x US-09-811-115-2 (1-3768)
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 US-09-811-115-2; Sequence 2, Application US/09811115; Patent No. US20020035736A1
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100.00%
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50.31%
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50.31%
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US-09-811-115-2
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Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 US-09-811-123-8
 Pred. No.:
 RESULT 5
 Score:
 Score:
 δ
 δŏ
 Sequence 5, Application US/10207498
Publication No. US203014356841
GENERAL INFORMATION:
APPLICANT: Elizabeth Singer
APPLICANT: Elizabeth Singer
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND MODULATING INTERACTION NUMBER: US/10/207,498
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/308,431
PRIOR PELLING DATE: 2001-07-27
 116 GACAAGGCUGCCCCGCCGAGAGAGACCACCCCCCCGAGCGUCC 160
 Sequence 8, Application US/09811123
Sequence 8, Application US/09811123
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: MTHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: MTHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: MTHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: MYHERE: 05/09/811,123
CURRENT APPLICATION NUMBER: 05/298,327
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PRIOR PILING DATE: 2000-10-05
PRIOR PELING DATE: 2000-10-05
PRIOR PELING DATE: 2000-06-23
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 3765
115
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Mismatches:
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 US-09-811-123-8
Query Match:
DB:
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Score:

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; Publication No. US2003015711941
; Fublication No. US2003015711941
; GEMERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TTLLE OF INVENTION: MTHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; TTLLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
; TILLE REFERENCE: 21012.1 483.23
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT APPLICATION NUMBER: US/10/313,644
; NUMBER OF SEQ ID NOS: 5
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 Sequence 5, Application US/09441411

Publication No. US20030008342A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scholler, Mathalie B.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: KARL ERIK
FILE REFERENCE: 730033.409
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFFWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
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50.31%
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 Alignment Scores:
Pred. No.:
 Alignment Scores:
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 Query Match:
 FEATURE
 Pred. No.:
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 Sequence 1, Application US/09930125
Publication No. US20020193329A1
Sequence 1, Application US/09930125
Publication No. US20020193329A1
SEMERAL INFORMATION:
APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.
APPLICANT: Ralos, Michael J.
APPLICANT: Moneill, Particia D.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
TITLE OF INVENTION: OF HER-2/NEU-BSSOCIATED MALIGNANCIES
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
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LOCATION: (2026)...(3765)
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LOCATION: (2968)...(3765)
OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2968)...(3144)
COTHER INFORMATION: preferred portion of the phosphorylation domain
OTHER INFORMATION: (delta PD) of human HER-2/neu
 3768
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 Length:
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Conservative:
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; LOCATION: (1)...(3765)
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 Alignment Scores:
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 US-09-854-356-9
 US-09-930-125-1
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 Query Match:
 Pred. No.:
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 Length:
Matches:
Conservative:
 Conservative:
 Mismatches:
 Mismatches:
 JUNC_SEQ3_SEQ5 (1-30) x US-10-146-473-32 (1-4473)
 JUNC_SEQ3_SEQ5 (1-30) x US-10-101-510-81 (1-4473)
 US-10-146-473-32
Sequence 32, Application US/10146473
Publication No. US20030108888A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Gout, IVan
APPLICANT: Grockert, Elisabeth
APPLICANT: Grockert, Elisabeth
APPLICANT: Grockert, Lloyd
APPLICANT: Chen, Yao-Teeng
APPLICANT: Chen, Yao-Teeng
APPLICANT: Chen, Yao-Teeng
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APPLICANT: Chen, Yao-Teeng
APPLICANT: Chen, Yao-Teeng
APPLICANT: Chen, Y
 Length:
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 Indels:
 100.00%
100.00%
50.31%
 0.0214
80.00
100.00%
100.00%
50.31%
 0.0214
80.00
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81
 TYPE: DNA; ORGANISM: HOMO SapienS
US-10-146-473-32
 Percent Similarity:
Best Local Similarity:
 Best Local Similarity:
 Percent Similarity:
 Alignment Scores:
 Alignment Scores:
 RESULT 9
US-10-101-510-81
 Query Match:
 Query Match:
 Pred. No.:
 Pred. No.:
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Sequence 11, Application US/09877177
Publication No. US20020192652A1
GENERAL INFORMATION
GENERAL INFORMATION:
TATLE OF INVENTION: Method of determining Epidermal Growth
TITLE OF INVENTION: Factor Receptor and HER2-New Gene Expression
FILE REFERENCE: 11220/120
CURRENT APPLICATION NUMBER: US/09/877,177
CURRENT FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSEQ for Windows Version 4.0
 Sequence 44, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401c1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
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Mismatches:
Indels:
 Matches:
Conservative:
Mismatches:
Indels:
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100.00%
100.00%
50.31%
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100.00%
100.00%
50.31%
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
 US-10-007-926A-119
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LENGTH: 4473
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 SEQ ID NO 11
 Query Match:
 Pred. No.:
 RESULT 13
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) NAME/KEY: CDS
; LOCATION: (151)..(3915)
; OTHER INFORMATION:
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ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Alignment Scores:
 LENGTH: 4530
 US-10-338-730-1
 SEQ ID NO 1
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Sequence 119, Application US/10007926A

Publication No. US20030143539A1

GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOUGATTE, REMI
APPLICANT: HOUGATTE, REMI
APPLICANT: HOUGATTE, REMI
APPLICANT: WIRNBAUM, DANIEL
APPLICANT: VIENS, PATRICE
TATLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT APPLICATION NUMBER: 06/254,090
PRIOR PAPLICATION NUMBER: 60/254,090
PRIOR PAPLICATION UNBER: 60/254,090
PRIOR PAPLICATION NUMBER: 60/254,090
PRIOR PAPLICATION NUMBER: 06/254,090
PRIOR PAPLICATION NUMBER: 06/254,090
PRIOR PAPLICATION NUMBER: 100/212-08
SOFTWARE: PALENTING DATE: 2000-12-08
SOFTWARE: PALENTING DATE: 2000-12-08
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SOFTWARE: PALENTING DATE: 2000-12-08
SEQ ID NO 119
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 TYPE: DNA

FERTURE:

FERTURE:

OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral

OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived

OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
 Sequence 124, Application US/10101510
| Publication No. US20030148295A1
| GENERAL INPORMATION:
| APPLICANT: WAN, JACKSON
| APPLICANT: WAN, JACKSON
| APPLICANT: WANG, YIXIN
| TITLE OF INVENTON: EXPERESION PROFILES AND METHODS OF USE
| FILE REFERENCE: 15117.0012
| CURRENT APPLICATION NUMBER: US/10/101,510
| PRIOR PILLING DATE: 2002-03-20
| PRIOR PILLING DATE: 2001-03-20
| NUMBER OF SEQ ID NOS: 805
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 124
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 Length:
Matches:
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Mismatches:
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Conservative:
Mismatches:
Indels:
 JUNC_SEQ3_SEQ5 (1-30) x US-10-007-926A-119 (1-4530)
 JUNC_SEQ3_SEQ5 (1-30) x US-10-101-510-124 (1-4530)
 Gaps:
 0.0217
80.00
100.00%
100.00%
50.31%
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80.00
100.00%
100.00%
50.31%
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-124
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 US-10-007-926A-119
 US-10-101-510-124
 Alignment Scores:
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 Score:
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4530
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 Length:
Matches:
Conservative:
Mismatches:
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 Sequence 1, Application US/10338730
| Publication No. US20030147905A1
| GENERAL INFORMATION:
| APPLICANT: Genzyme Corporation
| APPLICANT: Genzyme Corporation
| APPLICANT: Nicolette, Charles A.
| TITLE OF INVENTION: THERAPEUTIC COMPOUNDS
| FILE REFERENCE: 5017
| CURRENT APPLICATION NUMBER: US/10/338,730
| CURRENT FILING DATE: 2003-01-08
| PRIOR FILING DATE: 2002-03-16
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PatentIn version 3.1
 Indels:
 Search completed: October 17, 2003, 03:53:03 Job time: 39.0111 secs
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100.00%
100.00%
50.31%
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 SOFTWARE PATENTIAN STATES # 1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03.5EPT-1998
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: JUGGG, Linda R. 2,702
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAS: 650-324-0860
 GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVEWIION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
US-09-167-322-4
US-09-527-481-1
US-08-229-515A-14
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US-08-451-947-7
US-08-451-390-7
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US-08-451-947-9
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-146-283-3
; Sequence 3, Application US/09146283
; Patent No. 5976546
 TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
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Sequence 9, Appli
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-344-195-3
US-09-776-251-3
US-08-776-251-10
US-08-756-211-11
US-08-356-786-1
US-09-048-804-1
US-09-048-804-1
US-09-048-804-1
US-09-225-515A-9
US-08-229-515A-9
US-08-28-515A-9
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Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
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Perfect score:
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 Searched:
 Run on:
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 COUNTY: USA

COUNTY: USA

COUNTY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATORIN RC-DOS/MS-DOS

SOFTWARE: PATORIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/344,195

FILING DATE: 24-Jun-1999

CLASSIFICATION: <Unknown>
 APPLICANT: Laus, Reiner
Ruegg, Curtis L.
Rueggy
Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene;
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 GM-CSF-HER-2 fusion gene; Fig.
 Conservative:
Mismatches:
Indels:
 NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
 1976 GCACCGCCGCTCGCCCAGCCCCAGCACA 2005
 JUNC_SEQ3_SEQ5 (1-30) x US-08-579-823A-3 (1-2385)
 21 GlyProAla --- SerProLeuAspSerThr 29
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03.5EPT-1998
ATTORNEY/AGENT INPORMATION:
 Matches:
 Gaps:
 Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL INFORMATION:
 LENGTH: 2385 base pairs
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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52.83%
 CITY: Palo Alto
 ; INDIVIDUAL ISOLATE:
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 ANTI-SENSE: NO ORIGINAL SOURCE:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
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 US-09-344-195-3
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 Query Match:
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 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
 APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Ruegg, Curtis L.
APPLICANT: Ruegg, Curtis L.
TITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
) ORGANISM: homo sapiens
) INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
US-09-146-283-3
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
 Length:
Matches:
Conservative:
Mismatches:
 1976 GCACCCGCCCGCTCGCCCAGCACA 2005
 JUNC_SEQ3_SEQ5 (1-30) x US-09-146-283-3 (1-2385)
 21 GlyProAla -- SerProLeuAspSerThr 29
 Indels:
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
 7636-0010
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 3, Application US/08579823A Patent No. 6080409
 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
 LENGTH: 2385 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 0.0053
84.00
70.00%
70.00%
52.83%
 ORGANISM: homo sapiens
 650-324-0960
TYPE: nucleic acid
STRANDEDNESS: double
 linear
 Palo Alto
 Percent Similarity:
Best Local Similarity:
Query Match:
 GENERAL INFORMATION:
 ORIGINAL SOURCE:
ORGANISM: homo
 ORIGINAL SOURCE:
 ANTI-SENSE: NO
 ANTI-SENSE: NO
 HYPOTHETICAL:
 94306
 S
 Alignment Scores:
 CITY: Pal
STATE: CL
COUNTRY:
 US-08-579-823A-3
 ..
0
 RESULT 2
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 셤
 à
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Sequence 10, Application US/08776251
Patent No. 6025340
GENERATION:
APPLICANT: Springer, Caroline J
APPLICANT: Marais, Richard
TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug thera
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ECKET, David J.
TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
FILE REFERENCE: IBISO009
CURRENT APPLICATION NUMBER: US/09/200,355
CURRENT APPLICATION NUMBER: 1998-11-25
NUMBER OF EQ. ID NOS: 4
SOFTWARE: Patentin Version 3.1
SEQ ID NOS: 4
SEQ 10 NOS: 4
SEQ 10 NOS: 4
 STATE: VIGGILIDA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIALE

COMPUTER: TEM PC COMPATIALE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACHALIN Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION NUMBER: US/08/776,251

PHIOR APPLICATION NUMBER: PCT/GB95/01782

PHIOR APPLICATION NUMBER: PCT/GB95/01782

PRIOR APPLICATION NUMBER: GB 9415167.7

FILING DATE: 37-JUL-1995

PRIOR APPLICATION NUMBER: GB 9415167.7

FILING DATE: 27-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: ALTURE CARACTER NUMBER: 620-20

INFORMATION FOR SEQ ID NO: 10:

CENTIFICE CHARACTERISTICS:
 201
15
0
0
0
0
 ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
 Conservative:
 Mismatches:
 Length:
Matches:
 JUNC_SEQ3_SEQ5 (1-30) x US-09-200-355-3 (1-201)
 Indels:
 Sequence 3, Application US/09200355 Patent No. 6451524
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80.00
100.00%
100.00%
50.31%
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STRANDEDNESS: single
TOPOLOGY: linear
 TYPE: RNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-776-251-10
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 US-08-776-251-10
 US-09-200-355-3
 US-09-200-355-3
 Pred. No.:
 Score:
 qq
 APPLICANT: Springer, Caroline J
APPLICANT: Marals, Richard
TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
 CUTY: ALILIBYCUI
STATE: Virginia
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Name: PC-DOS/MS-DOS
SOFTWARE: Patentin Name: US/08/776,251
FILING DATE: 31-3NN-1997
FILING DATE: 31-3NN-1997
FILING DATE: 27-3UL-1995
FILING DATE: 27-3UL-1995
FILING DATE: 27-3UL-1994
FILING DATE: 27-3UL-1994
FILING DATE: 27-3UL-1994
FRIOR APPLICATION NUMBER: GB 9415167.7
FILING DATE: 27-3UL-1994
FRIOR AFPLICATION NUMBER: GB 9415167.7
FRIENG DATE: 27-3UL-1994
FRIENGENCE/DOCKET NUMBER: 620-20
INFORWATION FOR SEQ ID NO: 3:
CCANTENT CHARACTERISTICS:
 AUDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 1976 GCACCCGCCCGCCCCAGCCCCACCA 2005
 JUNC_SEQ3_SEQ5 (1-30) x US-09-344-195-3 (1-2385)
 21 GlyProAla --- SerProLeuAspSerThr 29
 JUNC_SEQ3_SEQ5 (1-30) x US-08-776-251-3 (1-153)
 Gaps:
 Sequence 3, Application US/08776251
Patent No. 6025340
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80.00
100.00%
100.00%
50.31%
 0.0053
84.00
70.00%
70.00%
52.83%
 SEQUENCE CHARACTERISTICS:
LENGTH: 153 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 ; MOLECULE TYPE: CDNA
US-08-776-251-3
 linear
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 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 US-08-776-251-3
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 Query Match:
Pred. No.:
 RESULT
 g
 q
 ö
 õ
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Query Match:

RESULT 7

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```
APPLICANT: Huston, James S.
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker
NUMBER OP SEQUENCES: 16
CORRESPONDENCE ADDRESS: 1
STREET: Exchange Place, 53 State Street
 1915 GACAAGGGCTGCCCCCCCCGCGAGAGACCCAGCCCTCTGACGTCC 1959
 APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
1915 GACAAGGGCTGCCCCGCCGAGCAGAGGCCAGCCCTCTGACGTCC 1959
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING APPLICATION: 424
PRIOR APPLICATION NUMBER: US/08/356,786
FILING APPLICATION NUMBER: US/08/356,786
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PICCHET DEAMUNG.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
REFERENCE/COCKET NUMBER: 27,829
REFERENCE/COCKET NUMBER: 27,829
RELEPRAK: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMOTH: 378 DASE PAIRS
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 /note= "product = "cerB-b2""
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-08-356-786-1
: Sequence 1, Application US/08356786
; Patent No. 5877305
 Sequence 1, Application US/09048804
Patent No. 5968748
GENERAL INFORMATION:
 80.00
100.00%
100.00%
50.31%
 TYPE: nucleic acid
STRANDEDNESS: single
 STREET: Exchange Plac
CITY: Boston
STATE: Massachusetts
 NAME/KEY: CDS
LOCATION: 1..3768
OTHER INFORMATION:
 MOLECULE TYPE: CDNA
 linear
 GENERAL INFORMATION:
 Best Local Similarity:
Query Match:
 COUNTRY: USA
 Percent Similarity:
 Alignment Scores:
 US-09-048-804-1
 US-08-356-786-1
 GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 93 GACAAGGGCTGCCCCGCCGAGCAGAGCCAGCCCTCTGACGTCC 137
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 ZIP: 98104-/Uyz
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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OFFRANTING SYSTEM:
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OFFRANTING STATEMENT 3768
15
 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 Length:
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 JUNC_SEQ3_SEQ5 (1-30) x US-08-776-251-10 (1-816)
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; Sequence 1, Application US/08625101
; Patent No. 5869445
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50.31%
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50.31%
 TYPE: nucleic acid
STRANDEDNESS: single
 STREET: 6300 Colun
CITY: Seattle
STATE: Washington
 TOPOLOGY: linear
 RY: USA
98104-7092
 Percent Similarity:
Best Local Similarity:
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 Percent Similarity:
Best Local Similarity:
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 ; LOCATION:
US-08-625-101-1
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 COUNTRY:
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Score:

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 Sequence 9, Application US/08229515A
Sequence 10. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
APPLICANT: RAZIUDDIN
APPLICANT: RAZIUDDIN
TITLE OF INVENTION: BERBZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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 COMPUTER TEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
RAPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
 Conservative:
Mismatches:
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Mismatches:
 JUNC_SEQ3_SEQ5 (1-30) x US-08-229-515A-9 (1-4530)
 JUNC_SEQ3_SEQ5 (1-30) x US-09-056-105-26 (1-4473)
 ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
 Length:
Matches:
 Indels:
 ATTORNEY/AGENT INFORMATION:
NAME: PERFYANA, DAVID 6
REGISTRATION UNBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
 Sequence 9, Application US/08645865; Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
 TELECOMMUNICATION INFORMATION: TELEPHONE: 404-688-0770
 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 4530 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
 80.00
100.00%
100.00%
50.31%
 100.00%
100.00%
50.31%
 0.0462
 Percent Similarity:
Best Local Similarity:
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 usa
 ZIP: 30303
 Alignment Scores:
 US-08-229-515A-9
 US-08-229-515A-9
 COUNTRY:
 RESULT 12
US-08-645-865-9
 Query Match:
 Query Match:
 ò
 a
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
 Sequence 26, Application US/09056105

Patent No. 6287569

GENERAL INPORMATION:
APPLICANT: WILPS, THOMAS J.
APPLICANT: WILPS, THOMAS J.
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER PILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 4473
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 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: 1MB C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/048,804
FILING DATE: Herewith
CLASSIFICATION:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ3_SEQ5 (1-30) x US-09-048-804-1 (1-4473)
 Length:
 ALTONALS FOLIA.

NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: 1SIS-2913
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3139
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4473 base pairs
 ATTORNEY/AGENT INFORMATION:
 0.0454
80.00
100.00%
100.00%
50.31%
 0.0454
 TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
US-09-048-804-1
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-056-105-26
 COUNTRY: U.S.A. ZIP: 19103
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
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 US-09-056-105-26
 Pred. No.:
 Pred. No.:
 Score:
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junc\_seq3\_seq5.rni

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 2065 GACAAGGGCTGCCCCGCCGAGAGAGACCAGCCCTCTGACGTCC 2109
 ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Suite 1800, Two Penn Center Plaza CITY: Philadelphia
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBAZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEDPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
 4530
15
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
 APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. Brigland, James M.
TITLE OF INVENTION: CANCER VACCINE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
 JUNC_SEQ3_SEQ5 (1-30) x US-08-645-865-9 (1-4530)
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
 Gaps:
 ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
 Sequence 4, Application US/09167322 Patent No. 6365151 GENERAL INFORMATION:
 80.00
100.00%
100.00%
50.31%
 LENGTH: 4530 base pairs
 TELEFAX: 404-688-9880 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 USA
 STATE: PA
 Percent Similarity: .
Best Local Similarity:
 Georgia
 COUNTRY:
 STREET: 127 Per CITY: Atlanta STATE: Georgia COUNTRY: usa
 CLASSIFICATION:
 30303
 TOPOLOGY:
 Alignment Scores:
 US-09-167-322-4
 US-08-645-865-9
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 Pred. No.:
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 Score:
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Mismatches:
Indels:
 Conservative:
Mismatches:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <UNKNOWN:

ATTORNEY/AGENT INFORMATION:

NAME: MONACO, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 7933-33 PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEPHONE: (215) 568-8383

TELEPHONE: (215) 568-5549

INFORMATION FOR SEQ. ID NO: 4:

SEQUENCE CHARACTERISTICS:
 Sequence 1, Application US/09527487
Patent No. 6528060
GENERAL INFORMATION:
TTYLE OF INFORMATION:
FILE REFERENCE: 126881309200
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILIG DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
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 0.0462
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; LOCATION: (151)..(3915)
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ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
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 US-09-167-322-4
 US-09-527-487-1
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 Query Match:
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 Pred. No.:
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Search completed: October 16, 2003, 17:16:18 Job time : 14.6049 secs

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Mouse Her-2/neu extracellular-phosphorylation domain fusion cDNA.
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; mouse; gene therapy; gene; ss.
and is derived by analysis of the total score distribution
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 ABA92250
ABK10730
ABL91709
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AAA09455
 AAD43935
AAD43986
 ABV78168
AAD32743
 ABQ83856
AAF24297
 AAA14815
 AAT40739
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 AAA14812
 AAT01585
 ABK83918
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 AAZ31071
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(without alignments)
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame_plus_p2n model

 159
1 DKGCPAEQRASPLTSQNEDLGPASPLDSTF 30
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 Maximum Match 100%
Listing first 45 summaries
 October 15, 2003, 21:06:28
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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 BLOSUM62
 Total number of
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 Minimum DB
Maximum DB
 OM protein
 Sequence:
 Searched:
 Database
 Run on:
 Title:
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Nucleotide Sequenc Human tyrosine kin Human gene express Breast carcinoma r Human HERZ-neu SEQ

Breast cancer asso Human Her2/Neu enc HER2 transgene pla HER2 transgene pl Human HER2 (ExbB2) Human breast and o

luman cDNA for Human cDNA

Human gene express Human Her-2 DNA. Her-2/neu (ERBB2/c Human HER2 gene.

Human tumour antig HER-2 nucleic acid

Sequence encoding cDNA encoding the

Human HER-2/neu on Human heregulin 2 Human HER-2/neu pr Human ERBB2 polynu Human ERBB2 Dolynu

Human HER-2 cDNA.

Human HER-2/neu co CDNA encoding huma HER-2/neu oncogene

DNA encoding a wil Her2 normal form t

Humanised vector p DC8scFv-erbB2EC fu

Her2-GM-CSF immuno

Mouse Her-2/neu ex Her-2/neu extracel

Description

Human Her2 antigen Human ERBB2 DNA SE Human Her-2/neu cD Human Her-2/neu cD Human her-2/neu bN Human her-2/neu bN

Her-2/neu extracellular-phosphorylation domain-TcP0 fusion cDNA.

17-JUN-2002 (first entry)

oncogene; cancer; tumour; vaccine; tyrosine kinase;

Her-2/neu;

```
The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAMSIIS). The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of human cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vacines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the ECD of Her-2/neu is fused to a manner esponse to Her-2/neu is fused to a minan or PD (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by cannot encoding the fusion protein, with a nucleic acid color concert. Specific T-cells are useful for inhibiting the development of a cancer. Specific T-cells are useful for inhibiting the development of a cancer. Specific T-cells that specifically react with a Her-2/neu in a patient. T cells that specifically react with a Her-2/neu for the anner of the anner
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 inhibit the development of cancer in a patient.
 Sequence 2763 BP; 571 A; 855 C; 772 G; 565 T; 0 other;
 /product= "Her-2/neu ECD-PD fusion"
 Conservative:
Mismatches:
 1978 GGCCCCTCCAGCCCCATGGACACCTTC 2007
 Length:
Matches:
 GlyProAlaSerProLeuAspSerThrPhe 30
 Indels:
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 JUNC_SEQ3_SEQ5 (1-30) x ABA92252 (1-2763)
 Disclosure; Fig 23; 141pp; English.
 ABA92253 standard; cDNA; 2781 BP
 1,16e-10
144.00
100.00%
83.33%
 3-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
 Cheever MA, Gheysen D;
 phosphorylation domain
 WPI; 2002-241743/29.
P-PSDB; AAM51152.
 (CORI-) CORIXA CORP.
 Percent Similarity:
Best Local Similarity:
 WO200212341-A2
 Alignment Scores:
 14-FEB-2002
 ABA92253;
 21
 Query Match:
 ABA92253
 RESULT
 Score:
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Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (ECD) and the phosphorylation domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAM51151) plus a -cterminal TCPO motif that improves immunogenicity. The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of numan cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu vercines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the ECD of Her-2/neu is fused to a Her-2/neu intracellular domain or PD (or its DeltaPD fragment). An immune response to Her-2/neu protein in the form of a vaccine, or by carnoffecting cells of an animal ax vivo with a nucleic acid cells che nording the fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. The luston protein in the form of a vostate cancer in a patient.
 /product= "Her-2/neu ECD-PD-TcP0 fusion"
 Sequence 2781 BP; 574 A; 859 C; 779 G; 569 T; 0 other;
 Length:
Matches:
Conservative:
Mismatches:
 receptor; TcP0; mouse; gene therapy; gene; ss
 Indels:
 (CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Location/Qualifiers 1..2781
 Disclosure; Fig 25; 141pp; English.
 1.17e-10
144.00
100.00%
83.33%
90.57%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
 - Mus musculus.
 /*tag=
 Cheever MA, Gheysen D;
 phosphorylation domain
 WPI; 2002-241743/29.
 Similarity:
 P-PSDB; AAM51153
 WO200212341-A2.
 Percent Similarity:
 Alignment Scores:
 14-FEB-2002.
 Chimeric
 Query Match:
 Best Local
```

JUNC\_SEQ3\_SEQ5 (1-30) x ABA92253 (1-2781)

Length: Matches: Conservative: Mismatches:

m

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Sequence 69 BP; 13 A; 26 C; 20 G; 10 T; 0 other;
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Query Match:
DB:
 Pred. No.:
 Score:
 g
 염
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
 A nucleic acid molecule (AAT72725) codes for a fusion protein (AAM19764) comprising granulocyte-macrophage colony stimulating factor (GM-CSF) and Herz, a growth factor receptor that is over-expressed in breast and ovarian cancer cells. It was prepd. by PCR amplification of Herz cDNA from a breast cancer cell line and fusion to GM-CSF CNNA. Fusion expression vectors can be used to transfect mammalian and insect cells. The Herz-GM-CSF fusion protein is used to generate anti-Herz immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the
 Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in a
 Her2-GM-CSF; granulocyte macrophage colony stimulating factor;
growth factor receptor; oncogene; immunostimulant; cancer;
therapy; ss.
 Sequence 2385 BP; 488 A; 780 C; 677 G; 440 T; 0 other;
 /*tag= a
/product= GM-CSF-Her2 fusion protein
 Her2-GM-CSF immunostimulant fusion protein DNA
 1978 GGCCCTCCAGCCCCATGACACCATC 2007
 GlyProAlaSerProLeuAspSerThrPhe 30
 /product= Leu-Glu linker
1976..2359
 .ocation/Qualifiers
 (ACTI-) ACTIVATED CELL THERAPY INC.
 Disclosure; Fig 8; 45pp; English.
 BP
 /*tag= d
/product= GM-CSF
 'product= Her2
 AAT72725 standard; cDNA; 2385
 95US-0579823.
 96WO-US20241
 1970..1975
 (first entry)
 /*tag= b
 υ
 11..1969
 . 2359
 /*tag=
 Mu
 WPI; 1997-363674/33.
 Laus R, Ruegg CL,
 vertebrate subject
 P-PSDB; AAW19764
 fusion protein.
 Homo sapiens
 W09724438-A1
 23-DEC-1996;
 28-DEC-1995;
 17-SEP-1997
 10-JUL-1997
 21
 AAT72725;
 mRNA
 mRNA
 mRNA
 Key
 RESULT
 셤
 à
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The present sequence encodes a peptide of wild type erbB-2 receptor protein, where the splicing event occurs. An alternatively spliced variant of erbB-2 receptor protein, designated SPLICE erbB-2 receptor protein, designated SPLICE erbB-2 receptor protein, has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The conserved cysteine residues, compared to the unspliced protein. The carbb-2 polynucleotide is used to construct probes for detecting a list of a seam of the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the
 ij
 cancer;
 Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
 SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
 DNA encoding a wild type erbB-2 receptor protein fragment.
 1976 GCACCGCCCGCCCCAGCCCCAGCACA 2005
 21 GlyProAla --- SerProLeuAspSerThr 29
 [ndels:
 central nervous system and wound healing.
 JUNC_SEQ3_SEQ5 (1-30) x AAT72725 (1-2385)
 Example 2; Fig 3B; 60pp; English.
 AAA14815 standard; cDNA; 69
 99WO-CA00912.
 98US-0165192
84.00
70.00%
70.00%
52.83%
 08-AUG-2000 (first entry)
 Siegel PM;
 (UYMC-) UNIV MCMASTER
 WPI; 2000-303768/26.
 wound healing; ss.
 P-PSDB; AAY84681
 WO200020579-A1
 Homo sapiens.
 01-OCT-1999;
 02-OCT-1998;
 13-APR-2000.
 Muller WJ,
 AAA14815;
 AAA14815
```

Fri

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The HER2 proto-oncogene encodes a tyrosine kinase receptor, which functions in cellular signal transduction. The HER2 protein is functions in cellular signal transduction. The HER2 protein is functions in cellular signal transduction. The HER2 protein is two forms: a normal form and a truncated form. The present sequence is the normal form RNA of HER2. The truncated form RNA sequence of HER2 (AAA6126) encodes a protein associated with increased resistance to the growth inhibiting effects of a monoclonal antibody, Herceptin, used in cancer treatment. The truncated form of the transcript contains unique structures not found in the normal form. The present sequence is predictive of Herceptin-resistant canner and detection of the present sequence may therefore be used as a method of diagnosing breast cancer. Other diseases which may be identified by using a similar method to detect other RNA molecules are hyperproliferative conditions, Lupus, erythematosus, psoriasis, inflammation, cardiovascular disease, pain, arthritis, obesity, trauma, Huntingdon's disease or neurological
 /bound_moiety= "her2 normal form transcript bases"
/note= "Forms double-stranded region with bases 137-152
of Her2 normal form transcript"
 Identifying a target nucleic acid sequence predictive of preselected disease states such as a cancerous state, by comparing members of a set of mRNA molecules, from a common gene, containing different sequences
/note= "Forms double-stranded region with bases 172-187 of Her2 normal form transcript" 154..166
 201
15
0
0
0
0
 G; 44 U; 0 other;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 JUNC_SEQ3_SEQ5 (1-30) x AAA62125 (1-201)
 Example 2; Fig 3; 38pp; English.
 Sequence 201 BP; 34 A; 67 C; 56
 AAV21727 standard; cDNA; 2125
 99WO-US27710.
 98US-0110024.
 80.00
100.00%
100.00%
50.31%
 0.00714
 E
 17-AUG-1998 (first entry)
 /*tag= m
172..187
 /*tag= n
 (ISIS-) ISIS PHARM INC.
 WPI; 2000-400027/34.
 Best Local Similarity:
 WO200031110-A1.
 and structures
 Percent Similarity:
 misc_binding
 22-NOV-1999;
 25-NOV-1998;
 Alignment Scores:
 25-NOV-1998;
 02-JUN-2000
 disorders.
 stem_loop
 Scker DJ;
 116
 AAV21727;
 Query Match:
 9
 RESULT
 Score:
 XXXX
 /bound_molety= "Her2 normal form transcript bases"
/note= "Forms double-stranded region with bases 111-117
of Her2 normal form transcript"
 /*tag= f // The control of the contr
 /bound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 74-75
of Her2 normal form transcript"
 /bound_moiety= "her2 normal form transcript"
/note= "Forms double-stranded region with bases 84-90
of Her2 normal form transcript"
 /bound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 58-59
of Her2 normal form transcript"
 /bound_molety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 78-81
of Her2 normal form transcript"
 Her2; disease prediction; breast cancer; human; tyrosine kinase; ss.
 /bound_moiety= "Her2 normal form transcript bases"
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 0000
 Length:
Matches:
Conservative:
 Mismatches:
 Indels:
 Location/Qualifiers
 JUNC_SEQ3_SEQ5 (1-30) x AAA14815 (1-69)
 AAA62125 standard; RNA; 201
 Her2 normal form transcript.
 100.00%
100.00%
50.31%
 00195
 (first entry)
 ø
 /*tag= k
137..152
/*tag= 1
 80.00
 .117
 94..107
 /*tag=
 8..18
/*tag=
37..56
/*tag=
58..59
 /*tag=
74..75
 /*tag=
 /*tag=
 /*tag=
 *tag=
 *tag=
 Best Local Similarity:
 Percent Similarity:
 Alignment Scores:
 20-JUN-2001
 Homo sapiens
 misc_binding
 misc_binding
 misc_binding
 misc_binding
 misc_binding
 misc_binding
 misc_binding
 stem_loop
 stem_loop
 stem_loop
 stem_loop
 stem_loop
 AAA62125;
 Query Match:
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 RESULT 5
 AAA62125
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AAZ50586
 RESULT
 Plasmid pITL-HHER2/neu comprises base vector pITL (see AAV21724) and a human HER-2/neu nucleic sequence. pITL-HHER2/neu was used to evaluate the toxicity of anti-tumour vaccination in rats, and in phase I and phase II trials to evaluate polynucleotide vaccination advanced breast cancer. Novel humanised vectors, which can be based on pITL, comprise a human-derived promoter or mammalian nonloque which is functional in mammalian target tissue and cells and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells but are capable of extended stable expression of the target sequence, generating an immune response in immunised individuals. The vectors selectively alloit immune responses to the target sequences with little or no immune response to the corporates.
 Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
 /*tag= b
/oote= "combined splice and polyA sequences"
1195..1401
 Vector; vaccine; tumour; antigen; plasmid pITL-hHER/neu; human; HER-2/neu; C-erbB-2; breast cancer; ds.
 2125
15
0
0
0
0
 598 G; 428 T; 0 other;
 origin of replication"
 Conservative:
Mismatches:
Indels:
Gaps:
 Length:
Matches:
 /product= human HER-2/neu
922..1181
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 /note= "RANTES promoter
 Example 7; Page 41-42; 125pp; English.
 Location/Qualifiers
13..921
 /*tag= c
/note= "SupF gene"
1412..1864
 Sequence 2125 BP; 449 A; 650 C;
 Humanised vector pITL-hHER/neu
 /*tag= d
/note= "ColE1
 Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
Synthetic.
 97WO-US14306
 96US-0023931
 0.124
80.00
100.00%
100.00%
50.31%
 1877..2125
 ..1181
 /*tag=
 Nelson PJ;
 WPI; 1998-159552/14.
 Best Local Similarity:
 of the vectors
 Percent Similarity
 misc_feature
 WO9806863-A1
 14-AUG-1997;
 14-AUG-1996;
 Alignment Scores:
 19-FEB-1998
 Nelson EL,
 polyA_site
 promoter
 Query Match:
 ..
8
 CDS
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DC8 scFv; single-chain variable fragment; erbB2EC; extracellular domain; human; fusion construct; tetramerisation domain; constant domain; heterominibody; multifunctional compound; melanoma; sarcoma; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; antiproliferative; prevention; treatment; malignant; haematopoietic cell; lymphoma; leukaemia; solid tumour; carcinoma; ds.
 New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis
 DC8scFv-erbB2EC fusion construct containing tetramerisation domain.
 /*tag= f
/note= "5' end of human IgG3 upper hinge region
with 3 additional nucleotides"
808..924
 67..390
/*tag= c
/label= DC8scFv_light_chain_variable_region
 *tag= e
label= DC8scFv_heavy_chain_variable_region
 *tag= a
product= "DC8scFv-erbB2EC fusion protein"
 ij,
 *tag= g
label= Human_p53_tetramerisation_domain
 Zettl
 label= Glycine-Serine-linker_DNA
 Baeuerle PA, Borschert K,
 (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG
 /*tag= h
/label= Short_peptide_linker
 /*tag= b
/label= Leader_sequence
 label = erbB2EC_domain
 Location/Qualifiers
 /label= His_tag
AAZ50586 standard; DNA; 2871
 99WO-EP05416.
 98EP-0114082
 23-MAY-2000 (first entry)
 2845..2862
 946..2844
 ..771
 ..945
 ..807
 1..435
 - Unidentified.
- Homo sapiens.
 ..2865
 /*tag=
 /*tag=
 *tag=
 Kufer P, Dreier T,
 WPI; 2000-195265/17.
P-PSDB; AAY44993.
 WO200006605-A2
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 28-JUL-1999;
 28-JUL-1998;
 10-FEB-2000
 sig_peptide
 AAZ50586;
 Chimeric
 Chimeric
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JUNC\_SEQ3\_SEQ5 (1-30) x AAV21727 (1-2125)

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01-NOV-2000; 2000US-0704232.
 Query Match:
 ABK8620"
 RESULT
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 The patent discloses heterominibodies which are multifunctional compounds produceable in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains, where one of the polypeptide chains comprises, a CH1-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, an immunoglobulin light chain). The polypeptide chains further comprise, the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and conferent (poly)peptides lack an intrinsic affinity for one another and cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, and processed to the continumas.
 The present sequence is a fusion construct comprising DC8 single-chain FV (scFV) fragment at the N-terminus, extracellular domain of human erbB2 at the C-terminus and a tetramerisation domain between them. This construct was prepared to find out whether an oligomerisation domain characterised in bacterial expression system is applicable for expression of fully functional and secretable recombinant protein in mammalian host cells. This tetrameric construct was not expressed as secretable and fully functional protein in mammalian cells. Hence general applicability of the tetramerisation domain for oligomerisation strategies in mammalian cells was ruled out.
 Human, HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
breast cancer; prostate cancer; ovarian cancer; lung cancer;
colon cancer; ds.
 2797 GACAAGGCTGCCCGCCGAGCAGCAGCCAGCCCTCTGACGTC 2841
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 2871 BP; 598 A; 868 C; 834 G; 571 T; 0 other;
 Length:
Matches:
Conservative:
 /*tag= a
/product= "HER-2/neu protein"
 Mismatches:
 Indels:
 JUNC_SEQ3_SEQ5 (1-30) x AAZ50586 (1-2871)
 Location/Qualifiers
 Example 9; Fig 49; 166pp; English.
 Human HER-2/neu coding sequence.
 Bb
 AAA89736 standard; DNA; 3600
 99US-0117976.
 0.179
80.00
100.00%
100.00%
50.31%
 28-JAN-2000; 2000WO-US02164
 (first entry)
 1..3600
 /*tag=
 Best Local Similarity:
 WO200044899-A1
 Percent Similarity:
 Homo sapiens
 29-JAN-1999;
 Alignment Scores:
 12-JAN-2001
 03-AUG-2000
 AAA89736;
 Query Match:
 ..
No.:
 AAA89736
 RESULT
 Score
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cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepadnavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 The present sequence encodes the human HER-2/neu protein. HER-2/neu is
 a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 /*tag= a
/product= "Breast cancer antigen Her2 variant"
 Sequence 3600 BP; 723 A; 1108 C; 1075 G; 694 T; 0 other;
 cDNA encoding human breast cancer antigen, Her2 variant.
 3600
15
0
0
0
 Human; Her2; cytostatic; antiviral; immunostimulant;
 Conservative:
Mismatches:
 Length:
Matches:
 Indels:
 JUNC_SEQ3_SEQ5 (1-30) x AAA89736 (1-3600)
 Location/Qualifiers
7..3678
 Disclosure; Fig 15; 128pp; English.
 ABK86207 standard; cDNA; 3678 BP.
 01-NOV-2001; 2001WO-US45626.
 100.00%
100.00%
50.31%
 SMIK) SMITHKLINE BEECHAM.
 WPI; 2000-505976/45.
P-PSDB; AAB21198, AAB21208.
 24-SEP-2002 (first entry)
 0.235 \\ 80.00
 Cheever MA, Gheysen D;
(CORI-) CORIXA CORP
 prostate cancers -
 Best Local Similarity:
 these neoplasias
 WO200240059-A2
 Percent Similarity:
 Homo sapiens
 Alignment Scores:
 23-MAY-2002
 ABK86207;
```

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Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbB2) protein (AAW0111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Lys676-Vall255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral vector, for genetic immunisation of an animal.
 HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
malignancy; treatment; tumour; ss.
 DNA encoding HER-2-neu poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/neu oncogene is
 /note= "region which elicits immune response"
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 Conservative:
Mismatches:
 Length:
Matches:
 Indels:
 /*tag= a
/product= "HER-2/neu"
 JUNC_SEQ3_SEQ5 (1-30) x AAT40739 (1-3768)
 Socation/Qualifiers
 Claim 1; Page 49-56; 71pp; English.
 /note= "oncogene"
2026..3765
/*tag= b
 ВР
 AAX01912 standard; DNA; 3768
 Human HER-2/neu oncogene DNA
 96WO-US01689
 95US-0414417
 0.248
80.00
100.00%
 21-APR-1999 (first entry)
 50.31%
 UNIW) UNIV WASHINGTON.
 ..3768
 Disis ML;
 WPI; 1996-455361/45.
 Best Local Similarity:
 P-PSDB; AAW01111
 Percent Similarity:
 Homo sapiens.
WO9630514-A1
 28-MAR-1996;
 31-MAR-1995;
 misc_feature
 03-OCT-1996.
 Cheever MA,
 Alignment Scores:
 associated
 AAX01912;
 Query Match:
 RESULT 11
 AAX01912
 Score:
 g
 à
 The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example tumnour cells or vitally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynuclectide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer. The method can be used to treat prostate cancer, as well as lymphomas and celucated and pancreatic cancer, as well as lymphomas and infections such as those caused by hepadnaviruses, lentviruses (including human immunodeficiency virus (HIV)), herpesviruses and the cancer and present sequence represents the coding sequence of human breast cancer antigen, Her2 variant, used as a target antigen in the method of the invention.
 by
of
 Inducing a cell-mediated immune response against a target antigen, reducing undesized cells and stimulating presentation of an antigen a cell, comprises administering a polynucleotide encoding a variant an antigen
 /note= "nucleotides 2026-3765 (claim 1) code for HER-2/neu intracellular domain"
 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
 3678
115
0
0
0
0
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 AMERICAN FOUND BIOLOGICAL RES INC. MINCHEFF M S. LOUKINOV D I.
 Disclosure; Page 128-134; 146pp; English.
 Gaps:
 Zoubak S;
 JUNC_SEQ3_SEQ5 (1-30) x ABK86207 (1-3678)
 Location/Qualifiers
 AAT40739 standard; cDNA; 3768 BP.
 DI,
 0.241
80.00
100.00$
100.00$
50.31$
 (first entry)
 1..3765
/*tag=
 Mincheff MS, Loukinov
 WPI; 2002-527524/56.
P-PSDB; AAU98923.
 HER-2/neu oncogene.
 Percent Similarity:
Best Local Similarity:
 ZOUBAK S.
 Homo sapiens.
 Alignment Scores:
 01-JAN-1997
 (MINC/)
 AAT40739
 AMBI-)
 ZOUB/)
 Query Match
```

Score:

AAT40739

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The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human protated with cancers (i.e. self-proteins), for example, human protated specific membrane antigen (PSM) herequin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APC3) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 Thelper cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and channed CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human contracts.
 tumor associated
 Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostated cancer
 Leach D,
 Antigen-presenting cell; immunogenic; immune response; Hi
oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other:
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 Conservative:
 Mismatches:
Indels:
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/product= "HER-2/neu protein"
 Matches:
 Length:
 Claim 62; Page 187-193; 220pp; English.
 Mouritsen S, `Nielsen KG,
3irk P, Karlsson G;
 Human HER-2/neu protein encoding DNA
 JUNC_SEQ3_SEQ5 (1-30) x AAA09455 (1-3768)
 Location/Qualifiers
1..3768
 AAH23392 standard; DNA; 3768 BP
 21-JAN-2000; 2000US-0177545
 19-JAN-2001; 2001WO-US01850
 0.248
80.00
100.00$
100.00$
50.31$
 (first entry)
 (MEBI-) M & E BIOTECH AS
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 Birk P,
 Best Local Similarity:
 P-PSDB; AAY92620
 WO200153463-A2
 Percent Similarity:
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 Homo sapiens
 25-SEP-2001
 26-JUL-2001
 Steinaa L,
 Gautam A,
 AAH23392;
 Query Match:
 RESULT 13
 Score:
 δ
 This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a mailgnancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
 ဌ
 Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated mallgnancy, particularly for treating or
 Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Human heregulin 2 (Her2) coding sequence.
 Claim la; Column 23-32; 26pp; English
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93US-0106112.
95US-0414417.
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 99WO-DK00525
 96US-0625101
 (first entry)
 (UNIW) UNIV WASHINGTON.
 Cheever MA, Disis ML;
 WPI; 1999-152835/13.
 preventing tumours
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAW92406
 WO200020027-A2.
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 01-APR-1996;
 17-MAR-1993;
12-AUG-1993;
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 05-OCT-1998;
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US5869445-A
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 09-FEB-1999
 13-APR-2000
 20-0CT-1998
 AAA09455;
 1915
 Query Match:
 RESULT 12
 AAA0945
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Score:

g

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NAME OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART O

HER-2/neu;

Page

junc\_seq3\_seq5.rng

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Score:
 Pred
 \mathbf{x} \times \mathbf{y} \times
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 g
 The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER.2/neu protein. The antigen-presenting cells are useful as vaccines for elliciting or enhancing an immune response to HER.2/neu protein, particularly in treating or preventing malignancies in which the HER.2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER.2/neu protein (also known as p185 or c-erbB2).
 protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
 Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target -
 useful
 or
 New antigen-presenting cells, useful as vaccines for eliciting o
enhancing an immune response to HER-2/neu protein, particularly
for treating or preventing cancer, e.g. breast cancer
 1915 GACAAGGCCTCCCCCCCGAGCAGCAGCCAGCCTCTGACGTCC 1959
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
15
0
0
0
 Conservative:
 Mismatches:
Indels:
 Length:
Matches:
 Hadwiger
 Human ERBB2 polynucleotide SEQ ID NO 52.
 Gaps:
 JUNC_SEQ3_SEQ5 (1-30) x AAH23392 (1-3768)
 Claim 1; Page 41-46; 49pp; English.
 Rost S,
 ВР
 Hand-Zimmermann S;
 ABZ35744 standard; DNA; 3768
 09-JAN-2001; 2001DE-1000588
 09-JAN-2001; 2001DE-1000588
 0.248
80.00
100.00%
100.00%
50.31%
 (first entry)
 ŝ
 (RIBO-) RIBOPHARMA AG.
 WPI; 2002-683450/74.
 WPI; 2001-476112/51
 Limmer
(CORI-) CORIXA CORP
 Best Local Similarity:
Query Match:
 P-PSDB; AAB85458
 Percent Similarity:
 DE10100588-A1
 Homo sapiens
 Alignment Scores:
 07-FEB-2003
 Cheever MA,
 18-JUL-2002.
 Kreutzer R,
 ABZ35744;
 No.:
 RESULT 14
 Score:
 Pred.
g
 ü
 à
```

```
CC The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide compairs. At least part of one strand (S1, S2) of the ds structures in each cof dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded CC method uses antisense inhibition of gene expression using double stranded cor infections, especially by plasmodium or viruses/viroids (pathogenic or humans, animals or plants). The method provides more effective inhibition CC of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the
 Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.
 This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded
 ρχ
 introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon
 1915 GACAAGGGCTGCCCCGCCGAGCAGAGCCAGCCCTCTGACGTCC 1959
 15
 T; 0 other;
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 3768
15
0
0
0
 Length:
Matches:
Conservative:
Mismatches:
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719
 Hadwiger
 Indels:
 Disclosure; Page 43-44; 98pp; German.
 JUNC_SEQ3_SEQ5 (1-30) x ABZ35744 (1-3768)
Claim 13; Page 38-39; 100pp; German.
 Human ERBB2 DNA fragment SEQ ID 52.
 s,
 BP.
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 Rost
 09-JAN-2001; 2001DE-1000587
 09-JAN-2001; 2001DE-1000587
 0.248
80.00
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100.00%
 23-JAN-2003 (first entry)
 50.31%
 Limmer S,
 (RIBO-) RIBOPHARMA AG.
 WPI; 2002-742209/81.
 Best Local Similarity:
 DE10100587-C1.
 Percent Similarity:
 Homo sapiens
 Alignment Scores:
 21-NOV-2002.
 Kreutzer R,
 ABX09987;
 Query Match:
 RESULT 15
 ABX09987
```

```
(ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) pototaln genes, particularly oncogenes, cytokine genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX0936-ABX10075 represent gene fragments used to illustrate the method of the invention.
```

Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;

|                   | 3768       | 15       | 0                   | 0                      | 0            | 0     |
|-------------------|------------|----------|---------------------|------------------------|--------------|-------|
|                   | Length:    | Matches: | Conservative:       | Mismatches:            | Indels:      | Gaps: |
|                   | 0.248      | 80.00    | 100.00%             | 100.00%                | 50.31%       | 24    |
| Alignment Scores: | Pred. No.: | Score:   | Percent Similarity: | Best Local Similarity: | Query Match: | DB:   |

JUNC\_SEQ3\_SEQ5 (1-30) x ABX09987 (1-3768)

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Search completed: October 15, 2003, 23:48:41 Job time: 31.4941 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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 PAT 18-MAR-2002
 PAT 18-MAR-2002
 Her-2/neu fusion proteins
Patent: WO 0212341-A 28 14-FEB-2002;
CORIXA CORPORATION (US) ; SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualifiers
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synthetic construct
artificial sequences.
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artificial sequences.
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 ò
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Submittee (11-VV-Zuol) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
buring sequence assembly date is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone ame. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequencing problems, such
chemistry or covered by high quality data (i.e., pired quality) >-
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr;, TREMBL; Wp;, WORNPEP; Information on the WORNPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-355L10 is
from the RFOI-23 Mouse PAC Library
FOR further details see http://www.chori.org/bacpac/home.htm
 VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP23-355LIO it may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP23-355LIO is at 186134 in this sequence. The true right end of clone RP23-438D7 is at 2000 in this
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 big dye terminator reads only."
47794. .47812
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a 47900 c 47689 g 44258 t
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Phillimore, B.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 214019)
 Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 2, 2001 this sequence version replaced gi:12061538.
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 Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Contact: sequence_submissions@genome.wi.mit.edu
 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-16G14
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 Conservative:
Mismatches:
Indels:
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85.50
72.41%
62.07%
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 Mus musculus
 Unpublished
 Percent Similarity:
Best Local Similarity:
Alignment Scores:
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AC064803/c
 Pred. No.:
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TITLE
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AUTHORS
 TITLE
JOURNAL
 VERSION
KEYWORDS
SOURCE
 ACCESSION
 COMMENT
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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: M13; M77815; 54% of reads Sequencing vector: Plasmid; n/a: 46% of reads Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 208571 bases at least Q40 Consensus quality: 210746 bases at least Q30 Consensus quality: 210746 bases at least Q30 Insert size: 197000; agarose-fp Insert size: 127719; sum-of-contigs Quality coverage: 8: in Q20 bases; agarose-fp Quality coverage: 7:8 in Q20 bases
 contig of 21460 bp in length gap of 100 bp contig of 3285 bp in length contig of 3170 bp in length contig of 3170 bp in length gap of 100 bp
 100 bp
9 of 12575 bp in length
f 100 bp
9 of 12222 bp in length
 f 100 bp
g of 8549 bp in length
f 100 bp
g of 39693 bp in length
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of 13991 bp in length
f 100 bp
of 16051 bp in length
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of 20603 bp in length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Direct Submission
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Submitted (20-NOV-2002) Hiroki Sasaki, Tsukiji 5-1 jl, Chuo-ku,
Research Inskitute, Genetics Division; Tsukiji 5-1 jl, Chuo-ku,
Tokyo 104-0045, Japan (E-mail: hksasaki@qan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
Location/Qualifiers
 Kuwahara,Y., Tanabe,C., Ikeuchi,T., Aoyaqi,K., Nishigaki,M., Sakamoto,H., Hoshinaga,K., Yoshida,T., Sasaki,H. and Terada,M. Presence of novel mechanisms other than the BFB cycles in amplification of human oncogene
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Direct Submission
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Research Institute, Genetics Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104-0045, Japan (E-mail:hksasaki@gan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
 Kuwahara,Y., Tanabe,C., Ikeuchi,T., Aoyagi,K., Nishigaki,M., Sakamnco,H., Hoshinaga,K., Yoshida,T., Sasaki,H. and Terada,M. Presence of novel mechanisms other than the BFB cycles in amplification of human oncogene
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 SOURCE
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Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) (ERBBZ) gene, complete cds.

AY208911. GI:27657999
 Direct Submission
Submitted (30-DEC-2002) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: http://egp.gs.washington.edu).
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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 ProAlaGlu------15
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Kuwahara,Y., Tanabe,C., Ikeuchi,T., Aoyagi,K., Nishigaki,M., Sakamoto,H., Hoshinaga,K., Yoshida,T., Sasaki,H. and Terada,M. Presence of novel mechanisms other than the BFB cycles in amplification of human oncogene Unpublished

2 (pass 1 to 20271)
 Direct Submission
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Research Institute, Genetics Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104-0045, Japan (E-mail:hksasakiégan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
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Research, 320 Charles Street, Cambridge, MA 02141, USA
BITTEN, Bastlen, V. Bloom, T., Bouguslavkiy, L., Boukhaalter, B.
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 Submitted (02-0CT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on oct 2, 2002 this sequence version replaced gi:22758800. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
 Contact: sequence_submissions@genome.wi.mit.edu
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Homo sapiens chromosome 17, clone RP11-94L15, complete sequence.
AC079199
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Conservative:
Mismatches:
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53.46%
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 Percent Similarity:
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 Pred. No.:
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KEYWORDS
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TITLE
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AC079199
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 AUTHORS
 SOURCE
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|---------------------------------------------------------------------|---------------|--------------------|--------------------------|-------------------------------------------|------------------------------------------|------------------------------|---------------|---------------|---------------|---------------|---------------|---------------------------------|--------------------------------------------------------------------------|---------------|---------------|---------------|---------------------------------|-----------------------------------------------|---------------|------------------------------------------------------|---------------------------------|---------------|-----------------------------------------------------------|-----------------------------------------|---------------|--------------------------|--------------------------|-----------------------|------------------------|---------------|----------------------------------------------------|---------------|---------------|---------------------------------------------------------|---------------|
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 161815<br>23<br>: 0<br>3 24<br>2                                                                                                 | GlnargalaSerProLeurhrser 15                                                                                            | 168585 bp DNA linear PRI 01-OCT-2002  6303  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.  15)  and Lander, E.  ome 17, clone CTD-2019C10  15)  Nusbaum, C., Lander, E., Abraham, H., Allen, N., J., Barna, N., Bastien, V., Bedå, F., hoehel, T., Colangelo, M., Collins, S., P., DeArellano, K., Dewar, K., Diaz, J.S., Doyle, M., FitzHugh, W., Gage, D., S., Ginde, S., Goyette, M., Graham, L., Maratas, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Landers, T., Lehoczky, J., Liu, G., Locke, K., Macdonald, P., Marquis, N., Liu, G., Locke, K., Macdonald, P., Marquis, N., P., McGurk, A., McGurk, M., McPheeters, R.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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Barra, N. Bastien, V. Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chang, J., Cheepel, Y., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardham, L., Grand-Pherre, N., Bagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Macdean, C., Macdonald, P., Major, J., Mathews, C., Macdonald, P., Major, J., Mathews, C., Norman, C., Norman, C., Phunkhang, P., Pierre, N., Naylor, J., Murphy, T., Naylor, J., Naylor, J., Mihova, T., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Voll, S., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Voll, S., Wu, X., Wyman, D., Young, G., Zainoun, J., Chaner, A., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Chaner, A., Limer, Liter, Submitted (01-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (barles Street, Cambridge, MA 02141, USA (barles Street, Cambridge, MA 02141, USA (barles) Nusbaum, C. Lander, E. Ali, A. Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boquslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Deward, S., Cooke, P., DeArellano, K., Deward, J., Cooke, P., DeArellano, K., Deward, J., Raratas, A., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Raratas, A., Kells, C., Landeres, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landeres, T., Levine, R., Jindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marthews, C., Mccarthy, M., Maylor, J., Marens, L., Milloo, M., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, J., Peterson, K., Phunkhang, P., Peterson, K., Phunkhang, P., Peterson, K., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vallmer, A. and Zody, M., Direct Submission
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 Submitted (01-0CT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA OO OCt 1, 2002 this sequence version replaced gi:22597589.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
 Only the last 167.6 kb of this clone are being submitted.
The remainder overlaps accession number AC097491 [WICGR project
L11967].
 Contact: sequence_submissions@genome.wi.mit.edu
 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
 Project Information
 Center project name: L8894
Center clone name: 2019_C_10
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TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Consensus quality: 19489 bases at least Q30
Consensus quality: 19489 bases at least Q30
Consensus quality: 194769 bases at least Q20
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Estimated insert size: 175000, agarose-fp estimation
Quality coverage: 9.72 in Q20 bases; sun-of-contigs estimation
Quality coverage: 9.72 in Q20 bases; sun-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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 Direct Submission
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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PAT 08-AUG-2001

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70.00%
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Unclassified.
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 PAT 14-FEB-2001
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
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 Laus, R., Ruegg, C. Landon. and Wu, H. Immunostimulatory compositions
Patent: US 5976546-A 3 02-NOV-1999;
Location/Qualifiers
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 Unclassified.
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PAT 24-NOV-2000

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Search completed: October 16, 2003, 11:01:09 Job time : 507.208 secs

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Mus musculus
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 (without alignments) 3105.423 Million cell updates/sec
 October 15, 2003, 22:47:19; Search time 234.794 Seconds
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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159
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Sequence:
 Scoring table:
 Total number
 OM protein
 Searched:
 Database
 Run on:
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Best Local Similarity:
Query Match:
 Percent Similarity:
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 BASE COUNT
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 Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 LysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGly:::|||||||
 Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
 618
18
3
5
3
 Mouse BAC End Sequences from Library RPCI-23
 1 (bases 1 to 422)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
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Conservative:
Mismatches:
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JOURNAL
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 AUTHORS
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 RESULT 2
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 KEYWORDS
 FEATURES
 COMMENT
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```
Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-HT0371-
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2 (bases 1 to 430)

 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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 Indels:
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 /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A min:-library was made by cloning products derived from OreStres Por (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under lissue mrNA and cONA amplification.
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0371-250
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NIH-WGC http://mgc.nci.nih.gov/.
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Shotgun sequencing of the human transcriptome with ORF expressed
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 AGENCOURT_14477527 NIH_MGC_181 Homo sapiens cDNA clone IMAGE:30396701 5', mRNA sequence.
CD558559.1 GI:31584627
EST.
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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85.00
46.00%
46.00%
53.46%
 Homo sapiens
 16 -----
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 Pred. No.:
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VERSION
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 JOURNAL
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CD558559
LOCUS
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Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE
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 COMMENT
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 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Trobs sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0371-180
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derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
 BF869854 378 bp mRNA linear EST 17-JAN-2001 IL3-ET0114-251000-317-B07 ET0114 Homo sapiens cDNA, mRNA sequence. BF869854
 Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvahlo, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 378)
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 Shotgun sequencing of the human transcriptome with ORF expressed
 Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Mismatches:
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 low stringency
136 c 13
 BF869854.1 GI:12259984
 Homo sapiens (human)
 rel: +55-11-2704922
 0.894
81.00
88.89%
88.89%
50.94%
 sequence tags
 sednence tags
 Homo sapiens
 Simpson, A.J.
 Best Local Similarity:
 Proc. Nat
20202663
 10737800
 83
 Percent Similarity:
 Brazil
 Alignment Scores:
 Query Match:
 source
 BF869854/c
 DEFINITION
 ..
9
 ACCESSION
VERSION
 BASE COUNT
 ORGANISM
 MEDLINE
PUBMED
 REFERENCE
 JOURNAL
 JOURNAL
 AUTHORS
 KEYWORDS
SOURCE
 RESULT 6
 FEATURES
 TITLE
 TITLE
 COMMENT
 ORIGIN
 Score:
 LOCUS
 Pred.
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 g
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 .
G
 Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-ET0114-
251000-31-7807&t3=2000-10-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 177.
Location/Qualifiers
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/clone_lib="ET0114"
/clone_logan: lung_tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
a 119 c 110 g 73 t
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Fobo
 Homo sapiens mRNA; EST DKFZp686K21213_r1 (from clone DKFZp686K21213)
 Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Han M., Wiemann S.;
 237 GACAAGGGCTGCCCCGCCGAGCAGCAGCCAGCCCTTTGACGTCC 193
 Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERWANY
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
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0
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09-MAY-2003 (Rel. 75, Last updated, Version 1)
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 standard; RNA; EST; 411
 EST; expressed sequence tag.
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100.00%
50.31%
 Tel: +55-11-2704922
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junc\_seq3\_seq4.rst

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/note="Organ: colon_est; Vector: pucl8; Site_l: Smal;
Site_l: Smal; A mini-library was made by cloning products
Site_l: Smal;
Site_l: Smal;
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
86 a 149 c 108 g 90 t.
 BG988031 450 bp mRNA linear EST 13-JUN-2001
MR2-HT1160-110101-005-a06 HT1160 Homo sapiens cDNA, mRNA sequence.
 Dias Net., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-CS0049-181000-202-A06&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 387.
Location/Qualifiers
 Email: asimpsonelouding.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HT1160-110101-005-a06&t3=2001-01-11&t4=1)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Shotgun sequencing of the human transcriptome with ORF expressed
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
 367 GACAAGGCTGCCCCGCCGAGAGAGACCAGCCCTCTGACGTCC 323
 12
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 433
15
0
0
0
 Conservative:
Mismatches:
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
 Matches:
 Indels:
 JUNC_SEQ3_SEQ4 (1-30) x BF762317 (1-433)
 BG988031
BG988031.1 GI:14392101
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80.00
100.00%
 Homo sapiens (human)
 (bases 1 to 450)
 rel: +55-11-2704922
 Fax: +55-11-2707001
 50.31%
 Homo sapiens
 Percent Similarity:
Best Local Similarity:
 10737800
 Alignment Scores:
 Query Match:
 source
 Pred. No.:
 DEFINITION
 ORGANISM
 SASE COUNT
 MEDLINE
PUBMED
 REFERENCE
 AUTHORS
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BG988031
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 JOURNAL
 KEYWORDS
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 VERSION
 TITLE
 COMMENT
 ORIGIN
 Score:
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 g
 /db_xref="taxon:9606"
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/clone=lib="666 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfilA + SfilB"
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 bF/62317 433 bp mRNA linear EST 12-JAN-2001 IL2-CS0049-181000-202-A06 CS0049 Homo sapiens CDNA, mRNA sequence. BF762317
 Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae; Homo.

1 (bases 1 to 433)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Wagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 \operatorname{Simpson}, A \cdot J \cdot Shotgun sequencing of the human transcriptome with ORF expressed
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project.
 This clone (DKF2p686K21213) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 411
15
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0
0
 BP; 70 A; 126 C; 125 G; 90 T; 0 other;
 Conservative:
Mismatches:
Indels:
 /tissue_type="cDNA-collection"
 sequence of the clone insert
 Length:
Matches:
 Laboratory of Cancer Genetics
 Email: asimpson@ludwig.org.br
 JUNC_SEQ3_SEQ4 (1-30) x HSM069572 (1-411)
 Location/Qualifiers
 BF762317.1 GI:12110217
 Contact: Simpson A.J.G.
 Homo sapiens (human)
 1.05
80.00
100.00%
100.00%
50.31%
 Fax: +55-11-2707001
 No s1 sequence available.
 Homo sapiens
 Best Local Similarity:
Query Match:
 the 5'
 Percent Similarity:
 Brazil
 Sequence 411
 Alignment Scores:
 EST
 DEFINITION
ACCESSION
VERSION
 source
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9
 RESULT 8
BF762317/c
 ORGANISM
 JOURNAL
MEDLINE
PUBMED
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 SOURCE
 Score:
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g ò

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/clone_lib="UI-E-E00"
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 Percent Similarity:
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 Query Match:
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 BASE COUNT
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80
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 DEFINITION
 ORGANISM
 ACCESSION
VERSION
 REFERENCE
AUTHORS
TITLE
JOURNAL
 KEYWORDS
SOURCE
 RESULT 11
 BI194790
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 COMMENT
 ORIGIN
 Pred.
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/dev_stage="Adult"
/clone_lib="HT1160"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
a 127 c 150 g 89 t
 EST 01-MAR-2002
 /dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
18-1319 335 8260
Fax: 319 335 9565
Email: bento-soareseulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Reverse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
 BM720186 466 bp mRNA linear EST 01-UI-E-E00-ahz-c-08-0-UI.rl UI-E-E00 Homo sapiens cDNA clone UI-E-E00-ahz-c-08-0-UI 5', mRNA sequence.
 Coordinated Laboratory for Computational Genomics
 450
115
0
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 Matches:
Conservative:
Mismatches:
Indels:
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 Length:
 Genome Res. 6 (9), 791-806 (1996)

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 Location/Qualifiers
 Location/Qualifiers
 JUNC_SEQ3_SEQ4 (1-30) x BG988031 (1-450)
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 BM720186.1 GI:19039265
 100.00%
100.00%
50.31%
 Homo sapiens (human)
 Contact: Soares, MB
 1.17
80.00
 Homo sapiens
 Percent Similarity:
Best Local Similarity:
 discovery
 97044477
8889548
 BM720186
 84
 Alignment Scores:
 EST.
 Query Match:
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 source
 LOCUS
DEFINITION
 BASE COUNT
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 Pred. No.:
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VERSION
KEYWORDS
SOURCE
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 AUTHORS
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 JOURNAL
 BM720186
FEATURES
 FEATURES
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/note="Organ: eys. Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-EFO0 is a cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dṛ)18 tail. The sequence tag for this library is CGGTATAÇC. This library was created for the program, Gene Discoveṭy in the Visual System, supported by National Eye Institute (NEI)."
 546 bp mRNA linear EST 10-JUL-2001 602948150F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5091396 5', BI194790
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
column: 13
High quality sequence start: 10
High quality sequence start: 10
High quality sequence stop: 495.
Location/Qualifiers
1. 546
 1 (bases 1 to 546)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 // Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo"
// Organism="Lakaton:960"
// Lissue_Lype="epithelioid carcinoma cell line"
// Lab_host="DHIOB (phage-resistant)"
// Clone_lib="NHH MGC_42"
// Orde="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
// Site_2: ECORX; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the
 15
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 466
115
0
0
0
 Matches:
Conservative:
Mismatches:
 Indels:
 Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 JUNC_SEQ3_SEQ4 (1-30) x BM720186 (1-466)
 BI194790.1 GI:14649810
 Homo sapiens (human)
 100.00%
 50.31%
```

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Percent Similarity:
Best Local Similarity:
Query Match:
 ø
 discovery
 97044477
8889548
 115
 Alignment Scores:
 EST.
 source
 BASE COUNT
ORIGIN
 No.:
 DEFINITION
 ORGANISM
 AUTHORS
TITLE
 RESULT 13
BM720098
 MEDLINE
PUBMED
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 JOURNAL
 FEATURES
 Score:
following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |" Life Technologies).
 1 (bases 1 to 547)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Washi-Merck EST Project 1997
 Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
 EST 03-JUN-1997
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 360.
Localion/Qualifiers
1. 547
/organism="Homo sapiens"
 AA443351 547 bp mRNA linear EST 03-JUN-1 zw85b05.rl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:783729 5' similar to gb:M11730 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (HUMAN);, mRNA sequence.
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 546
115
0
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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 AA443351
AA443351.1 GI:2156026
 Homo sapiens (human)
 1.49
80.00
100.00%
100.00%
50.31%
 Contact: Wilson RK
 Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Unpublished
 Alignment Scores:
 EST.
 LOCUS
DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Pred. No.:
 BASE COUNT
ORIGIN
 TITLE
JOURNAL
COMMENT
 REFERENCE
AUTHORS
 RESULT 12
 AA443351
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Cocation/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

1. 551

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/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
U1-E-E00 is a cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library
 EST 01-MAR-2002
 Coordinated Laboratory for Computational Genomics
University of Iowa
775 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
7761: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 561)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
 BM720098 561 bp mRNA linear EST 01-UI-E-EO0-ahz-c-05-0-UI.rl UI-E-EO0 Homo sapiens cDNA clone UI-E-EO0-ahz-c-05-0-UI 5', mRNA sequence.
 1 others
 547
115
0
0
0
 Conservative:
 Mismatches:
Indels:
 ų
 Length:
Matches:
 108
 Genome Res. 6 (9), 791-806 (1996)
 JUNC_SEQ3_SEQ4 (1-30) x AA443351 (1-547)
 ρ
 Genetics (www.resgen.com).
Seq primer: M13 Reverse.
 172
 BM720098
BM720098.1 GI:19039119
 Homo sapiens (human)
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80.00
100.00%
100.00%
50.31%
 Contact: Soares, MB
 υ
151
 Homo sapiens
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/clone="INAGE:296535"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH14MG_l7"
/note="Organ: muscle; Vector: pOTB7; Site_l: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_l: EcoRI;
/site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/NhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 AW410534 613 bp mRNA linear EST 29-JUN-2000 fh06h06.xl NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961635 5',
 con Library Preparation: Ling Hong/Rubin Laboratory
con Library Preparation: Ling Hong/Rubin Laboratory
con Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/Image/Amage.html
Plate: LLCM56 row: O column: 12
Plate: LLCM56 row: O column: 12
Plate: LLCM56 row: O column: 12
Cocation/Qualifiers
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 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini; Hominidaé; Homo. I bases 1 to 613)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 607
115
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15
0
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 Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 Matches:
 Matches:
 Length:
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 JUNC_SEQ3_SEQ4 (1-30) x BM083444 (1-607)
 JUNC_SEQ3_SEQ4 (1-30) x AW410534 (1-613)
 AW410534
AW410534.1 GI:6936075
 EST.
Homo sapiens (human)
Homo sapiens
 1.7
80.00
100.00%
100.00%
50.31%
 1.73
80.00
100.00%
100.00%
 50.31%
 mRNA sequence.
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 Query Match:
 Query Match:
 KEYWORDS
SOURCE
ORGANISM
 source
 DEFINITION
 Pred. No.:
 ACCESSION
VERSION
 AUTHORS
TITLE
 JOURNAL
COMMENT
 BASE COUNT
 REFERENCE
 RESULT 15
 AW410534
 FEATURES
 Score:
 ORIGIN
 Score:
 Livermore Livermore National Laboratory
Livermore Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact information on obtaining this clone, please contact
Info@image.lln.gov.
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Site_2: EcoRI; cDNA made by oligo-dT priming.
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 EST 16-NOV-2001
was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)." 171~{\rm c}-179~{\rm g}-113~{\rm t}-1 others
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 607)

Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and Prange, C. K.

The I.M. A. G. E. Consortium quality control effort: clone resequencing for verification
Unpublished
Other_ESTS: BE615590
Contact: Prange CK

The I.M. A. G. E. Consortium
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Sequence 125, Appli
Sequence 17, Appli
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Sequence 1132, Appli
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Sequence 13, Appli
Sequence 28706, A
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
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1. Sequence 3, Application US/10109213

2. Sequence 3, Application US/10109213

3. Publication No. US20020168670A1

3. GENERAL INFORMATION:

4. APPLICANT: ECKAT.

5. TILE OF INVENTION:

5. TILE REFERENCE: IBISO0099
12 US-10-207-498-5
9 US-09-811-123-8
9 US-09-811-123-8
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CURRENT FILING DATE: 2002-03-27
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PRIOR FILING DATE: 1998-11-25
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Sequence 2, Application US/09811115

BATCH NO. US2002035736A1

GENERAL INFORMATION:

APPLICANT: ELICKSON, Sharon

APPLICANT: ELICKSON, Sharon

APPLICANT: ELICKSON, ENDP

APPLICANT: King, Kathheen

TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL

FILE REFERENCE: GENENT.034A

CURRENT FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-03-16
 Sequence 9. Application US/09854356

Patent No. US20020177567A1

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Cheever, Martin A.

APPLICANT: COTIXE CORPORATION:

APPLICANT: SmithKline Beecham Biologicals S. A.

TITLE OF INVENTION: HER-2/neu Fusion Proteins

FILE REFERENCE: 014058-009810PC

CURRENT APPLICATION NUMBER: US/09/854,356

CURRENT APPLICATION NUMBER: US/09/854,356

CURRENT APPLICATION NUMBER: US 09/493,480

PRIOR APPLICATION NUMBER: US 09/493,480

PRIOR PILING DATE: 2000-01-28

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PRIOR FILING DATE: 1999-01-29
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 Sequence 5, Application US/10207498

Publication No. US20030143568a1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Elizabeth Singer

APPLICANT: Baif Landgraf

APPLICANT: David Eisenberg

TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING

TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3

FILE REFERENCE: 30448.103-US-10
 Sequence 8, Application US/09811123
Fatent No. US2002000158741
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
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 RESULT 2
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 g
 ð
 APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Copy, Teresa M.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: McNeill, Patricia D.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
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 APPLICANT: Hand-Zimmerman, Susan
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Sequence 1, Application US/10313644

Publication No. US2003015711941

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
APPLICANT: Hand-Zimmerman, Susan
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: WINDER: US/10/313,644
CURRENT APPLICATION NUMBER: US/10/313,644
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
 Sequence 5, Application US/09441411

Publication No. US20030008342A1

GENERAL INPORMATION:

APPLICANT: Scholler, Nathalie B.

APPLICANT: Disis, Mary L.

APPLICANT: Hellstrom, Ingegerd

APPLICANT: Hellstrom, Karl Erik

TITLE OF INVENTION: SUFFACE RECEPTOR ANTIGEN VACCINES

FILE REFERENCE: 730033.409

CURRENT APPLICATION NUMBER: US/09/441,411

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 26

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US-10-207-655-44

Sequence 44, Application US/10207655

Sequence 44, Application US/10207655

Sequence 44, Application US/10207655

Sequence 44, Application US/10207655

Sequence 44, Application US US/102076

SEQUENCAT: Ledbetter, Martha S.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

FILE REFERENCE: 390069.401C1

CURRENT PAILTAGING NUMBER: US/10/207,655

UNMBER OF SEQ ID NOS: 426

SOCTHARRE: Patentin version 3.0

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LENGTH: 4473
 Sequence 11, Application US/09877177
Publication No. US2002019265241
GENERAL INFORMATION:
APPLICANT: Peter V. Danenberg et al.
TITLE OF INVENTION: Factor Receptor and HER2-New Gene Expression
FILE REFERENCE: 11220/120
CURRENT FILING DATE: 2001-06-11
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Sequence 119, Application US/10007926A
Publication No. US20030143539A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: WIGNEN, CATHERINE
APPLICANT: VINCENT
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APPLICANT

 OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
 Sequence 124, Application US/10101510
Fublication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT APPLICATION NUMBER: 60/276,947
PRIOR PILING DATE: 2001-03-20
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SOFTWARE PATENTIN VET: 2.1
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 Sequence 1, Apsequence 1, Apsequence 1, Apsequence 1, Agsequence 1, Assequence 2, Assequence 2, Assequence 2, Assequence 2, Assequence 2, Assequence 1, Assequence 5, Assequence 7, Asse
 Sequence 1
Sequence 1
Sequence 1
Sequence 1
Sequence 1
 Sequence 7
Sequence 7
Sequence 9
 Sequence 3, Application US/09146283
Fatent No. 5976546
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
 COMPUTER: CA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION NUMBER: 75/09/146,283
FREGISTRATION NUMBER: 42,702
REGISTRATION NUMBER: 7636-0010.21
TELEPHONE: 650-324-0880
TELEPRANCE/DOCKET NUMBER: 7636-0010.21
TELEPRANCE/SOCKET NUMBER: 7636-0010.21
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US-09-677-1778-11

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Sequence 9, Appli
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 October 15, 2003, 22:55:19; Search time 7.60488 Seconds
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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 1 DKGCPAEQRASPLTSQNEDLGPASPLDSTF 30
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US-09-344-195-3
US-09-776-251-3
US-09-200-355-3
US-08-776-251-10
US-08-356-786-1
US-09-048-804-1
US-09-048-804-1
US-09-048-804-1
US-09-225-515A-9
US-08-229-515A-9
US-08-229-515A-9
 Total number of hits satisfying chosen parameters:
 US-09-146-283-3
 569978 seqs, 220691566 residues
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Listing first 45 summaries
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 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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 Length
 2385
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 Query
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Perfect score:
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880
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 Searched:
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ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
CLASSIFICATION: <UNKNOWN>
 œ
 Ruegg, Curtis L.
Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. US-08-579-823A-3
 Conservative:
Mismatches:
 REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
 1976 GCACCCGCCCGCTCGCCCAGCCCCAGCACA 2005
 JUNC_SEQ3_SEQ4 (1-30) x US-08-579-823A-3 (1-2385)
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
 Matches:
 Indels:
 Length:
 21 GlyProAla --- SerProLeuAspSerThr
 Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL INFORMATION:
 LENGTH: 2385 base pairs
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 TELEPHONE: 650-324-0880
 TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: 3:
 TYPE: nucleic acid
STRANDEDNESS: double
 SEQUENCE CHARACTERISTICS:
 APPLICANT: Laus, Reiner
 CORRESPONDENCE ADDRESS:
 84.00
70.00%
70.00%
52.83%
 ANTI-SENSE: NO
ORIGINAL SOURCE:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
 Alignment Scores:
 US-09-344-195-3
 US-09-344-195-3
 Pred. No.:
 Score:
 ŏ
 Q
 -- 1975
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
 GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegy, Curtis L.
APPLICANT: Ruegy, Curtis L.
TITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: 350 Cambridge Ave. Suite 250
STREET: 350 Cambridge Ave. Suite 250
STREET: CA
COUNTRY: USA
 1925 GACAAGGGCTGCCCCGCCGAGAGAGCCAGCCCTCTGACGTCCCTCGAG--
 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
 COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: JUGGW. Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010
TELEPHONIS. 650-324-0860
TELEPHONE: 650-324-0860
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 1976 GCACCGGCCGCTCGCCCAGCACA 2005
 JUNC_SEQ3_SEQ4 (1-30) x US-09-146-283-3 (1-2385)
 21 GlyProAla --- SerProLeuAspSerThr 29
 Sequence 3, Application US/08579823A Patent No. 6080409
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs
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84.00
70.00%
70.00%
52.83%
 ORGANISM: homo sapiens
 double
 double
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 TYPE: nucleic acid
STRANDEDNESS: doub
 nucleic acid
 Best Local Similarity:
 ANTI-SENSE: NO ORIGINAL SOURCE:
 STRANDEDNESS:
 ORIGINAL SOURCE:
 Percent Similarity:
 94306
 Alignment Scores:
 ORGANISM:
 ANTI-SENSE:
 US-08-579-823A-3
 US-09-146-283-3
 Query Match:
 . No. .
 RESULT 2
 Score:
 Pred.
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junc\_seq3\_seq4.rni

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US-08-776-251-10

Sequence 10, Application US/08776251

Sequence 10, Application US/08776251

Patent No. 6025340

GENERAL INFORMATION:

APPLICANT: Springer, Caroline J

APPLICANT: Marals, Richard

TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug thera

NUMBER OF SEQUENCES: 27
 Sequence 3, Application US/09200355
Patent No. 6451524
EMERRAL INFORMATION:
APPLICANT: Ecker, David J.
TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids FILE REFERENCE: IBIS0009
CURRENT APPLICATION NUMBER: US/09/200,355
CURRENT FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
 STATE: VITGINGS
STATE: VITGINGS
STATE: VITGINGS
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/776,251
FILING DATE: 31-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01782
FILING DATE: 27-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9415167.7
FILING DATE: 27-JUL-1994
ATTORNEY/ABGENT INPORMATION:
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 201
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 ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
 Length:
Matches:
Conservative:
Mismatches:
 JUNC_SEQ3_SEQ4 (1-30) x US-09-200-355-3 (1-201)
 Indels:
 NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
 INFORMATION FOR SEQ 1D NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 816 base pairs TYPE: nucleic acid STRANDEDNESS: single
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 100.00%
100.00%
50.31%
 REFERENCE/DOCKET NUMBER:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & V
 ORGANISM: Homo sapiens
 ; MOLECULE TYPE: CDNA
US-08-776-251-10
 TOPOLOGY: linear
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 SEQ ID NO 3
LENGTH: 201
 JS-09-200-355-3
 US-09-200-355-3
 TYPE: RNA
 Query Match:
 Pred. No.:
 g
 APPLICANT: Springer, Caroline J
APPLICANT: Marals, Richard
TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
WUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
 COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,251
FILING DATE: 31-JAN-1997
PRICA APPLICATION NUMBER: PCT/GB95/01782
FILING DATE: 27-JUL-1995
PRICA APPLICATION NUMBER: GB 9415167.7
FILING DATE: 37-JUL-1994
ATPORNEY/AGENT INFORMATION:
 153
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 ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
Length:
Matches:
Conservative:
Mismatches:
Indels:
 Conservative:
Mismatches:
 1976 GCACCCGCCCGCCCAGCCCCAGCACA 2005
 Length:
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 21 GlyProAla --- SerProLeuAspSerThr 29
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 Indels:
 Sequence 3, Application US/08776251
Patent No. 6025340
 NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620
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80.00
100.00%
100.00%
50.31%
 0.0053
84.00
70.00%
70.00%
52.83%
 LENGTH: 153 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: CDNA
 GENERAL INFORMATION:
 STATE: Virginia COUNTRY: USA
 CITY: Arlington
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 US-08-776-251-3
 us-08-776-251-3
 Query Match:
 Query Match:
 Pred. No.:
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Query Match:

RESULT 7

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APPLICANT: Huston, James S.
APPLICANT: Huston, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
CITY: Boston
STARE: Massachusetts
COUNTRY: USA
 Sequence 1, Application US/09048804
Patent No. S568748
GENERAL INFORMATION:
GAPPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
 1915 GACAAGGGCTGCCCCCCCGCGAGCAGAGCCAGCCCTCTGACGTCC 1959
 3768
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 /note= "product = "cerB-b2""
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
 Conservative:
Mismatches:
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 Matches:
 Indels:
 Length:
 FILING DATE:
CLASSIFICATION 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECHONGIS. (617) 248-7000
TELECHONE: (617) 248-7100
INFORMATION FOR SECIED NO: 1:
 Sequence 1, Application US/08356786
Patent No. 5877305
 100.00%
100.00%
50.31%
 LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 SEQUENCE CHARACTERISTICS:
 LOCATION: 1.3768
OTHER INFORMATION:
 TOPOLOGY: linear MOLECULE TYPE: CDNA
 Percent Similarity:
Best Local Similarity:
Query Match:
 GENERAL INFORMATION:
 NAME/KEY: CDS
 02109
 Alignment Scores:
 US-09-048-804-1
 US-08-356-786-1
 US-08-356-786-1
 Pred. No.:
 GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: OR CREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: OR OFFICE IS ASSOCIATED
OURBESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 1 ASpLysClyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 816
15
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 COMPUTER TELONALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
 Length:
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Conservative:
 Conservative:
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Indels:
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 ATTORREY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRAITON NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENOTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Length:
Matches:
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 Indels:
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 Gaps:
 Sequence 1, Application US/08625101
Patent No. 5869445
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100.00%
50.31%
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100.00%
100.00%
50.31%
 STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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 COUNTRY: USA
ZIP: 98104-7092
 Best Local Similarity:
 Best Local Similarity:
 Percent Similarity:
 Percent Similarity
 Alignment Scores:
Pred. No.:
 Alignment Scores:
Pred. No.:
 NAME/KEY:
 LOCATION:
US-08-625-101-1
 US-08-625-101-1
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Query Match:

Score:

S

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 2065 GACAAGGCTGCCCCCCCCGAGAGAGACCACCACCTCTGACGTCC 2109
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 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 9, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: BOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 4530
15
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
 Conservative:
Mismatches:
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Indels:
 JUNC_SEQ3_SEQ4 (1-30) x US-09-056-105-26 (1-4473)
 ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
 JUNC_SEQ3_SEQ4 (1-30) x US-08-229-515A-9 (1-4530)
 Length:
Matches:
 Indels:
 Sequence 9, Application US/08645865 Patent No. 5654406
 ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 141
 TELECOMMUNICATION INFORMATION: TELEPHONE: 404-688-0770
 TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
 100.00%
100.00%
50.31%
80.00
100.00%
100.00%
50.31%
 404-688-9880
 TYPE: nucleic acid
STRANDEDNESS: single
 GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 nsa
 30303
 TOPOLOGY:
 Alignment Scores:
 US-08-229-515A-9
 US-08-229-515A-9
 COUNTRY:
 US-08-645-865-9
 Query Match:
DB:
 Score:
 δλ
 . 엽
 Dp
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
UMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WU, YUNCI
TITLE OF INVENTION: PROCESSING
FILLE REFERENCE: 23,721
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER FILING DATE: 1997-04-10
EARLIER FILING DATE: 1997-04-10
MUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
 4473
 COMPUTER JAGE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: 18M PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/09/048,804
FILING DATE: Herewith
CLASSIFICATION:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ3_SEQ4 (1-30) x US-09-048-804-1 (1-4473)
 Gaps:
 ISIS-2913
 Sequence 26, Application US/09056105 Patent No. 6287569
 ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEFONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
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80.00
100.00%
100.00%
50.31%
 SEQUENCE CHARACTERISTICS:
LENGTH: 4473 base pairs
TYPE: Nucleic Acid
STRANDENESS: Single
TOPOLOGY: Unknown
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 TYPE: DNA
CRGANISM: Homo sapiens
US-09-056-105-26
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 Percent Similarity:
Best Local Similarity:
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US-09-048-804-1
 Alignment Scores:
Pred. No.:
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 US-09-056-105-26
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 Pred. No.:
 Score:
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ò 8 Φ

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APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STREET: Suite 1800, Two Penn Center Plaza
 ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
 4530
15
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 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
 Length:
Matches:
Conservative:
Mismatches:
 E: NEEDLE & ROSENBERG PC
127 Peachtree Street, Suite 1200
 JUNC_SEQ3_SEQ4 (1-30) x US-08-645-865-9 (1-4530)
 INT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
 [ndels:
 ATTORNEY/AGENT INFORMATION:
NAME: PERRYAAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
 Sequence 4, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
 100.00%
100.00%
50.31%
 LENGTH: 4530 base pairs
 404-688-9880
 80.00
 nucleic acid
EDNESS: single
 ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 COUNTRY: USA
 linear
 ADDRESSEE: NEEDL
STREET: 127 Peac
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
 Percent Similarity:
Best Local Similarity:
 STRANDEDNESS:
 Alignment Scores:
 CURRENT
 US-09-167-322-4
 US-08-645-865-9
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 Pred. No.:
 RESULT 13
 Score:
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δ g

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4530
15
0
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0
 Conservative:
Mismatches:
 Conservative:
Mismatches:
 NAME: MODACO, DELLEI A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 7933-33 PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-549

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 Sequence 1, Application US/09527487

Patent No. 6528060

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVOICTE, Charles

TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200
CURRENT APPLICANTION NUMBER: US/09/527,487

CURRENT FILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
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Matches:
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 Indels:
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 LENGTH: 4530 base pairs
 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
 TYPE: nucleic acid
STRANDEDNESS: single
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 100.00%
100.00%
50.31%
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; LOCATION: (151)..(3915)
US-09-527-487-1
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
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 SULT 15
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 Alignment Scores:
Pred. No.:
 Alignment Scores:
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 US-09-167-322-4
 US-09-527-487-1
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 FEATURE
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Search completed: October 16, 2003, 17:16:11 Job time: 15.6049 secs

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Human BRBB2 DNA SE
Human BRBB2 DNA SE
Human Her-2/neu DD
Human Her-2/neu DN
Human Her-2/neu DN
Human polynucleoti
Human BR2 (Ebb2)
Sequence encoding
 Breast cancer asso
Human Her2/Neu enc
HER2 transgene pla
HER2 transgene pla
Human HER2 (ErbB2)
Human breast and o
 Human HER-2/neu on
Human heregulin 2
Human HER-2/neu pr
Human ERBB2 polynu
Human ERBB2 DNA fr
 Human gene express
Human Her-2 DNA.
Her-2/neu (ERBB2/c
Human HER2 gene.
 DNA encoding a wil
Her2 normal form t
 Human HER-2/neu co
cDNA encoding huma
HER-2/neu oncogene
 Human tumour antig
HER-2 nucleic acid
 Breast carcinoma r
Human HER2-neu SEO
Human cDNA differe
 Her2-GM-CSF immuno
 Humanised vector p
DC8scFv-erbB2EC fu
 Human tyrosine kin
Human gene express
 Mouse Her-2/neu ex
 Her-2/neu extracel
 Nucleotide sequenc
 Human HER-2 cDNA.
 cDNA encoding the
 Human cDNA for
 Description
 Mouse Her-2/neu extracellular-phosphorylation domain fusion cDNA.
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; mouse; gene therapy; gene; ss.
and is derived by analysis of the total score distribution.
 ALIGNMENTS
 SUMMARIES
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AAD32743
ABA92250
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ABN85585
ABK83918
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AAD32746
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 Location/Qualifiers
1..2763
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 17-JUN-2002 (first entry)
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Query
Match Length D
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3768
 4473
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4530
 11115
1755
1767
 3600
 4299
 4472
 4473
 2871
 0.000
 Wus musculus
 Score
 RESULT 1
ABA92252
 Key
 Result
 Command line parameters:

WODEL-frame+_pol. DEV-xlp

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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-em
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 - nucleic search, using frame_plus_p2n model
 159 TORGCPAEQRASPLTSQNEDLGPASPLDSTF 30
 hits satisfying chosen parameters:
 2552756 seqs, 1349719017 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 October 15, 2003, 21:06:28
 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 JUNC_SEQ3_SEQ4
 BLOSUM62
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 Perfect score:
 Scoring table:
 Total number
 OM protein
 Database :
 Sequence:
 Searched:
 Run on:
 Title:
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junc\_seq3\_seq4.rng

Her-2/neu extracellular-phosphorylation domain-TcP0 fusion cDNA. Her-2/neu, oncogene, cancer; tumour; vaccine; tyrosine kinase; receptor; TcP0; mouse; gene therapy; gene; ss.

17-JUN-2002 (first entry)

Chimeric - Mus musculus Chimeric - Unidentified

```
The present sequence is that of cDNA encoding a fusion between with extracellular domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAMSIIS). The Her-2/neu gene is amplified and the oncoprotein is overaxpressed in a variety of human cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu vaccines comprising the fusion proteins or nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the ECD of Her-2/neu is fused to a confine to the intracellular domain or PD (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by canning the fusion protein, and delivering the transfected cells of an animal ex vivo with a nucleic acid and isolated specific T-cells are useful for inhibiting the development of a cancer in a patient. T cells that specifically react with a Her-2/neu cancer in a patient. T cells that specifically react with a Her-2/neu cancer in a patient. T cells that specifically react with a Her-2/neu cancer cancer in this interval of the cancer
 Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 order to inhibit the development of cancer in a patient.
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 Mismatches:
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Matches:
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 Indels:
 SMITHKLINE BEECHAM BIOLOGICALS.
 JUNC_SEQ3_SEQ4 (1-30) x ABA92252 (1-2763)
 Disclosure; Fig 23; 141pp; English.
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144.00
100.00%
83.33%
90.57%
 03-AUG-2001; 2001WO-US24283
 03-AUG-2000; 2000US-0632507
 Cheever MA, Gheysen D;
 phosphorylation domain
 WPI; 2002-241743/29.
P-PSDB; AAM51152.
 (CORI-) CORIXA CORP
 Percent Similarity:
Best Local Similarity:
 WO200212341-A2
 Alignment Scores:
 14-FEB-2002,
 1978
 21
 (SMIK)
 Query Match
g
 g
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```
Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain.
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAMSIISI) plus a C-terminal TCPO motif that improves immunogenicity. The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of numan cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu correlates with a poor prognosis. In preferred fusion proteins, the ECD of Her-2/neu intracellular domain or PD (or its Deltaph fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by cannistering the fusion protein in the form of a vaccine, or by administering the fusion protein in the form of a vaccine, or by concining the fusion protein, und delivering the transfected cells of an animal ex vivo with a nucleic acid of encoding the fusion protein, nucleic acids, and isolated concer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu encoding the fusion proteins, nucleic acids, and isolated concer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be unequed to protein a sample in
 inhibit the development of cancer in a patient.
 /product= "Her-2/neu ECD-PD-TcP0 fusion"
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 2781
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Conservative:
Mismatches:
Indels:
 Length:
 (CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Location/Qualifiers
1..2781
 Disclosure; Fig 25; 141pp; English.
 1.17e-10
144.00
100.00%
83.33%
90.57%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
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 Gheysen D;
 WPI; 2002-241743/29.
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 P-PSDB; AAM51153
 WO200212341-A2.
 Percent Similarity:
 Alignment Scores:
 Cheever MA,
 14-FEB-2002
 Query Match:
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JUNC\_SEQ3\_SEQ4 (1-30) x ABA92253 (1-2781)

ABA92253 standard; cDNA; 2781 BP

ABA9225

ABA92253;

m

Alignment Scores:

Pred. No.:

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1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
 A nucleic acid molecule (AAT72725) codes for a fusion protein (AAM19764) comprising granulocyte-macrophage colony stimulating factor (GM-CSF) and Her2, a growth factor receptor that is over-expressed in breast and ovarian cancer cells. It was prepd. by PCR amplification of Her2 CDNA from a breast cancer cell line and fusion to GM-CSF CDNA. Fusion expression vectors can be used to transfect mammalian and insect cells. The Her2-GM-CSF fusion protein is used to generate anti-Her2 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the
 Potent APC that activates T-cells to give multivalent cellular
Immune response - can also induce a cytotoxic T-cell response in a
 Her2-GM-CSF; granulocyte macrophage colony stimulating factor;
growth factor receptor; oncogene; immunostimulant; cancer;
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 Her2-GM-CSF immunostimulant fusion protein DNA.
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/product= Leu-Glu linker
1976..2359
/*tag= d
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 Location/Qualifiers
11..2359
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 Disclosure; Fig 8; 45pp; English.
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1970..1975
 96WO-US20241
 (first entry)
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 11..1969
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 vertebrate subject
 P-PSDB; AAW19764.
 fusion protein.
 23-DEC-1996;
 Homo sapiens
 W09724438-A1
 28-DEC-1995;
 17-SEP-1997
 therapy; ss.
 10-JUL-1997
 AAT72725;
 21
 mRNA
 mRNA
 MRNA
 SOS
 key
 RESULT
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Sequence 2385 BP; 488 A; 780 C; 677 G; 440 T; 0 other;

```
The present sequence encodes a peptide of wild type erbB-2 receptor protein, where the splicing event occurs. An alternatively spliced variant of erbB-2 receptor protein, designated SplicE erbB-2 receptor protein, has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The crbbs-2 polynucleotide is used to construct probes for detecting classorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SplicE erbB-2 in a sample. Agents ceg. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SplicE erbB-2 are useful for treating cancer. Substances which stimulate SplicE erbB-2 are useful for treating cancer. Substances which stimulate SplicE erbB-2 are useful for treating cancer since which stimulate splicE erbB-2 are useful for treating cancer. Substances which stimulate splicE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
 SPLICE erbB-2 receptor protein; cell transformation disorder; cancer; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
 Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
 DNA encoding a wild type erbB-2 receptor protein fragment.
2385
21
0
5
4
 Length:
Matches:
Conservative:
Mismatches:
 Sequence 69 BP; 13 A; 26 C; 20 G; 10 T; 0 other;
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 21 GlyProAla --- SerProLeuAspSerThr 29
 Indels:
 Gaps:
 JUNC_SEQ3_SEQ4 (1-30) x AAT72725 (1-2385)
 Example 2; Fig 3B; 60pp; English.
 BP
 AAA14815 standard; cDNA; 69
 99WO-CA00912.
 98US-0165192.
 (first entry)
 84.00
70.00%
70.00%
52.83%
 Siegel PM;
 (UYMC-) UNIV MCMASTER.
 WPI; 2000-303768/26.
 wound healing; ss.
 Best Local Similarity:
 P-PSDB; AAY84681.
 WO200020579-A1.
 Percent Similarity:
 Homo sapiens.
 08-AUG-2000
 01-OCT-1999;
 02-0CT-1998;
 13-APR-2000.
 Muller WJ,
 AAA14815;
 Query Match:
 AAA14815
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The HER2 proto-oncogene encodes a tyrosine kinase receptor, which functions in cellular signal transduction. The HER2 protein is functions in breast cancer. The HER2 receptor mRNA exists in at least two forms: a normal form and a truncated form. The present sequence is the normal form RNA of HER2. The truncated form RNA sequence of HER2 (AAA6126) encodes a protein associated with increased resistance to the growth inhibiting effects of a monoclonal antibody. Herceptin, used in cancer treatment. The truncated form of the transcript contains unique structures not found in the normal form. The present sequence is predictive of Herceptin-resistant cancer and detection of the present sequence may therefore be used as a method of diagnosing breast cancer. Other diseases which may be identified by using a similar method to detect other RNA molecules are hyperproliferative conditions. Lupus erythematosus, psoriasis, inflammation, cardiovascular disease, pain, arthritis, obesity, trauma, Huntingdon's disease or neurological
 /note=""Forms double-stranded region with bases 137-152 of Her2 normal form transcript"
 Identifying a target nucleic acid sequence predictive of preselected disease states such as a cancerous state, by comparing members of a set of mRNA molecules, from a common gene, containing different sequences and structures -
/note= "Forms double-stranded region with bases 172-187
of Her2 normal form transcript"
154..166
 /*tag= n
/bound_molety= "her2 normal form transcript bases"
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15
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0
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Mismatches:
Indels:
 Matches:
 Length:
 Gaps:
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 Example 2; Fig 3; 38pp; English.
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 17-AUG-1998 (first entry)
 E
 ...187
 (ISIS-) ISIS PHARM INC.
 /*tag=
 WPI; 2000-400027/34.
 Percent Similarity:
Best Local Similarity:
 WO200031110-A1
 misc_binding
 22-NOV-1999;
 Alignment Scores:
 25-NOV-1998;
 25-NOV-1998;
 02-JUN-2000
 disorders.
 stem_loop
 Ecker DJ;
 AAV21727;
 Query Match:
 9
 AAV21727
 Score:
 RESULT
 Pred.
 δ
 /bound_molety= "Her2 normal form transcript bases"
/note= "Forms double-stranded region with bases 111-117
of Her2 normal form transcript"
 /bound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 121-124
of Her2 normal form transcript"
 /bound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 74-75
of Her2 normal form transcript"
 /bound_molety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 58-59
of Her2 normal form transcript"
 /bound_molety= "her2 normal form transcript"
/note= "Forms double-stranded region with bases 84-90
of Her2 normal form transcript"
 / Cound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 78-81
of Her2 normal form transcript"
 Her2; disease prediction; breast cancer; human; tyrosine kinase; ss.
 /bound_moiety= "Her2 normal form transcript bases"
 0000
 Conservative:
Mismatches:
 Matches:
 Indels:
 Length:
 Location/Qualifiers
 JUNC_SEQ3_SEQ4 (1-30) x AAA14815 (1-69)
 AAA62125 standard; RNA; 201 BP
 Her2 normal form transcript.
 80.00
100.00%
100.00%
50.31%
 00195
 20-JUN-2001 (first entry)
 Q
 T
 Ø
 /*tag= k
137..152
 ...117
 121..124
 ..107
 3..18
/*tag=
 37..56
/*tag=
58..59
 /*tag=
 /*tag=
 /*tag=
 /*tag=
 *tag=
 *tag=
 /*tag=
 /*tag=
 /*tag=
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Homo sapiens
 misc_binding
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 misc_binding
 misc_binding
 misc_binding
 misc_binding
 misc_binding
 stem_loop
 stem_loop
 stem_loop
 stem_loop
 stem_loop
 AAA62125;
 Query Match:
 ..
No
 KESULT 5
```

junc\_seq3\_seq4.rng

112

BP.

(first entry)

scFv; single-chain variable fragment; erbB2EC; extracellular domain;

S

```
human; fusion construct; tetramerisation domain; constant domain; heterominibody; multifunctional compound; melanoma; sarcoma; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; antiporoliferative; prevention; treatment; malignant; haematopoletic cell; lymphoma; leukaemia; solid tumour; carcinoma; ds.
 DC8scFv-erbB2EC fusion construct containing tetramerisation domain.
 AA250586 standard; DNA; 2871
 WO200006605-A2
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 23-MAY-2000
 sig_peptide
 10-FEB-2000
 Chimeric
 AAZ50586
 Chimeric
 A CONTRACTOR OF A CONTRACTOR O
 Plasmid pITL-HBER2/neu comprises base vector pITL (see AAV21724) and a human HER-2/neu nucleic sequence. pITL-HHER2/neu was used to cavaluet the toxicity of anti-tumour vaccination in rats, and in phase I trials to evaluate polynucleotide vaccination in advanced breast cancer. Novel humanised vectors, which can be composed on pITL, comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and sequence acceptance site which accepts CDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells sequence, generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the target.
 Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
 /*tag- b
//tote- "combined splice and polyA sequences"
1195..1401
 Vector; vaccine; tumour; antigen; plasmid pITL-hHER/neu;
human; HER-2/neu; C-erbB-2; breast cancer; ds.
 Sequence 2125 BP; 449 A; 650 C; 598 G; 428 T; 0 other;
 /*tag= d
/note= "ColEl origin of replication"
 *tag= a
'product= human HER-2/neu
 /*tag= e
/note= "RANTES promoter'
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Example 7; Page 41-42; 125pp; English.
 Location/Qualifiers
13..921
 /*tag= c
'note= "SupF gene"
Humanised vector pITL-hHER/neu
 Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
 97WO-US14306
 96US-0023931
 ..1401
 412..1864
 ..2125
 Nelson PJ;
 WPI; 1998-159552/14.
 the vectors
 misc_feature
 14-AUG-1997;
 WO9806863-A1
 14-AUG-1996;
 19-FEB-1998
 Welson EL,
 Chimeric -
Synthetic.
 polyA_site
 promoter
 Vector;
 CDS
```

/note= "5, end of human IgG3 upper hinge region with 3 additional nucleotides" 808..924

/\*tag= g
label= Human\_p53\_tetramerisation\_domain

/\*tag= h /label= Short\_peptide\_linker 946..2844

. . 945

/\*tag= i /label= erbB2EC\_domain

2845..2862

/label= His\_tag

/\*tag= e label= DC8scFv\_heavy\_chain\_variable\_region

75..807

label- Glycine-Serine-linker\_DNA

O

\*tag=

391..435

\*tag= c label= DC8scFv\_light\_chain\_variable\_region

/\*tag= a /product= "DC8scFv-erbB2EC fusion protein"

Location/Qualifiers

. 2865

Unidentified..
 Homo sapiens.

/\*tag= b /label= Leader\_sequence

57..390

```
New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis \, -
 Zettl F;
 Borschert K,
 (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG
 Baeuerle PA,
 98EP-0114082
 Kufer P, Dreier T,
 WPI; 2000-195265/17.
P-PSDB; AAY44993.
28-JUL-1999;
 28-JUL-1998;
```

1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15

JUNC\_SEQ3\_SEQ4 (1-30) x AAV21727 (1-2125)

2125 15

Length: Matches:

Conservative: Mismatches: Indels:

0.124 80.00 100.00% 100.00% 50.31%

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

Q

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δλ
 QΩ
 produceable in a mammalian host cell as a secretable and fully functional heterodiamer of two polypeptide chains, where one of the polypeptide chains comprises. a CHI-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heterominibodies have octostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.
 The patent discloses heterominibodies which are multifunctional compounds
 The present sequence is a fusion construct comprising DC8 single-chain FV (scFV) fragment at the N-terminus, extracellular domain of human erbB2 at the C-terminus and a tetramerisation domain between them. This construct was prepared to find out whether an oligomerisation domain characterised in bacterial expression system is applicable for expression of fully functional and secretable recombinant protein in mammalian host cells. This tetrameric construct was not expressed as secretable and fully functional protein in mammalian cells. This tetrameric construct in mammalian cells. Hence general applicability of the tetramerisation domain for oligomerisation strategies in mammalian cells was ruled out.
 Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; ds.
 2797 GACAAGGGCTGCCCGCCGCGGAGAGACCAGCCCTCTGACGTCC 2841
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 2871 BP; 598 A; 868 C; 834 G; 571 T; 0 other;
 2871
15
0
0
0
 Matches:
Conservative:
 Mismatches:
 /product- "HER-2/neu protein"
 Length:
 Indels:
 JUNC_SEQ3_SEQ4 (1-30) x AAZ50586 (1-2871)
 Location/Qualifiers
 Example 9; Fig 49; 166pp; English.
 Human HER-2/neu coding sequence.
 AAA89736 standard; DNA; 3600
 99US-0117976.
 28-JAN-2000; 2000WO-US02164
 0.179
80.00
100.00%
100.00%
50.31%
 12-JAN-2001 (first entry)
 Ø
 1..3600
/*tag=
 Best Local Similarity:
 WO200044899-A1
 Percent Similarity:
 Homo sapiens.
 29-JAN-1999;
 Alignment Scores:
 03-AUG-2000
 AAA89736;
 Query Match:
DB:
 ..
8
 RESULT 8
 AAA89736
 Score:
 Pred.
ò
 g
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cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancfeatic cancer; lymphoma; leukaemia; hepadnavirus; lentivirus; herpesvirus; humannodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 HER-2/neu is
 a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or
 enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 /product= "Breast cancer antigen Her2 variant"
 The present sequence encodes the human HER-2/neu protein.
 Sequence 3600 BP; 723 A; 1108 C; 1075 G; 694 T; 0 other;
 cDNA encoding human breast cancer antigen, Her2 variant.
 3600
15
0
0
0
 cytostatic; antiviral; immunostimulant;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Gaps:
 JUNC_SEQ3_SEQ4 (1-30) x AAA89736 (1-3600)
 Location/Qualifiers
7..3678
 Disclosure; Fig 15; 128pp; English.
 ABK86207 standard; cDNA; 3678 BP
 01-NOV-2000; 2000US-0704232.
 01-NOV-2001; 2001WO-US45626
(CORI-) CORIXA CORP. (SMIK) SMITHKLINE BEECHAM.
 0.235
80.00
100.00%
100.00%
50.31%
 P-PSDB; AAB21198, AAB21208
 (first entry)
 ಠ
 Gheysen D;
 /*tag=
 WPI; 2000-505976/45
 prostate cancers -
 Percent Similarity:
Best Local Similarity:
Query Match:
 these neoplasias.
 WO200240059-A2
 Homo sapiens.
 Human; Her2;
 Alignment Scores:
 24-SEP-2002
 Cheever MA,
 23-MAY-2002
 ABK86207;
 Key
 ABK86207
 RESULT
 Score:
```

1

```
Human HER-2/neu oncogene CDNA (AAT40739) codes for HER-2/enu (p185 or c-erbb2) protein (AAW0111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or derequiated expression of an essentially normal gene product. Nucleotides 2026-3765 of the CDNA sequence code for the intracellular domain (Ly8676-Vall255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral
 HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
 DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
 /note= "region which elicits immune response"
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 Length:
Matches:
Conservative:
Mismatches:
 vector, for genetic immunisation of an animal.
 Indels:
 /*tag= a
/product= "HER-2/neu"
 JUNC_SEQ3_SEQ4 (1-30) x AAT40739 (1-3768)
 Location/Qualifiers
1..3768
 Claim 1; Page 49-56; 71pp; English.
 SS
 /note= "oncogene"
2026..3765
 ВР
 malignancy; treatment; tumour;
 AAX01912 standard; DNA; 3768
 Human HER-2/neu oncogene DNA
 95US-0414417.
 0.248
80.00
100.00%
100.00%
50.31%
 21-APR-1999 (first entry)
 UNIW) UNIV WASHINGTON
 /*tag=
 Cheever MA, Disis ML;
 WPI; 1996-455361/45.
 Percent Similarity:
Best Local Similarity:
 P-PSDB; AAW01111
 Homo sapiens.
WO9630514-A1
 28-MAR-1996;
 31-MAR-1995;
 Alignment Scores:
 misc_feature
 03-OCT-1996
 AAX01912;
 Query Match:
 RESULT 11
 Key
 AAX01912
 Score:
 셤
 δ
 The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example tumnour cells or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynuclectide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, orlorectal cancer and pancreatic cancer, as well as lymphomas and leukeamias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lentuviruses and the clausing human immunodeficiency virus (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present sequence represents the coding sequence of human breast cancer antigen, Her2 variant, used as a target.
 Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen by a cell, comprises administering a polynucleotide encoding a variant of
 /note= "nucleotides 2026-3765 (claim 1) code for HER-2/neu intracellular domain"
 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 AMERICAN FOUND BIOLOGICAL RES INC.
MINCHEFF M S.
LOUKINOV D I.
ZOUBAK S.
 Disclosure; Page 128-134; 146pp; English.
 Gaps:
 Mincheff MS, Loukinov DI, Zoubak S;
 JUNC_SEQ3_SEQ4 (1-30) x ABK86207 (1-3678)
 Location/Qualifiers
1..3765
 AAT40739 standard; cDNA; 3768 BP
 0.241
80.00
100.00%
100.00%
50.31%
 01-JAN-1997 (first entry)
 /*tag=
 WPI; 2002-527524/56.
P-PSDB; AAU98923.
 HER-2/neu oncogene.
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 Homo sapiens
 an antigen
 1825
 AAT40739;
 (AMBI-) / (MINC/) / (LOUK/) /
 (ZOUB/)
 Query Match:
 RESULT 10
```

Score: Pred

AAT40739

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3768 15 0 0 0 0

Dalum I;

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The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (PSEBb). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-iymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
 human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human
 Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
 Antigen-presenting cell; immunogenic; immune response; {\rm HER}^+2/{\rm neu}; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
 Haaning J, Leach
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
 115
0
0
0
 Conservative:
Mismatches:
 /*tag= a
/product= "HER-2/neu protein"
 Matches:
 Length:
 Indels:
 Claim 62; Page 187-193; 220pp; English.
 Nielsen KG,
 Human HER-2/neu protein encoding DNA.
 JUNC_SEQ3_SEQ4 (1-30) x AAA09455 (1-3768)
 Location/Qualifiers
 to treat prostate, prostate/breast SSM, FGF8b and Her2, respectively.
 BP
 en S, Niels
Karlsson G;
 AAH23392 standard; DNA; 3768
 19-JAN-2001; 2001WO-US01850
 21-JAN-2000; 2000US-0177545
 0.248
80.00
100.008
100.008
50.318
 (first entry)
 (MEBI-) M & E BIOTECH AS.
 1..3768
/*tag=
 Mouritsen (
Birk P, Ka
 WPI; 2000-349917/30
 Percent Similarity:
Best Local Similarity:
Query Match:
 P-PSDB; AAY92620
 WO200153463-A2
 sapiens
 Alignment Scores:
 25-SEP-2001
 26-JUL-2001
 Steinaa L,
 Gautam A,
 AAH23392;
 Homo
 RESULT 13
 AAH23392
 Score:
 Pred.
 ò
 g
 This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a mailgnancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
 t
 Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or preventing tumours
 Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 15
 Conservative:
Mismatches:
 Length:
Matches:
 Indels:
 Human heregulin 2 (Her2) coding sequence.
 Gaps:
 Claim la; Column 23-32; 26pp; English.
 JUNC_SEQ3_SEQ4 (1-30) x AAX01912 (1-3768)
 AAA09455 standard; DNA; 3768
 93US-0033644.
 96US-0625101
 96US-0625101
 95US-0414417
 99WO-DK00525
 98DK-0001261
98US-0105011
 0.248
80.00
100.00%
100.00%
50.31%
 10-AUG-2000 (first entry)
 (UNIW) UNIV WASHINGTON.
 Cheever MA, Disis ML;
 WPI; 1999-152835/13.
P-PSDB; AAW92406.
 Best Local Similarity:
 WO200020027-A2.
 Percent Similarity:
 17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
 Homo sapiens
 01-APR-1996;
 Alignment Scores:
 35-0CT-1999;
US5869445-A.
 01-APR-1996;
 05-OCT-1998;
20-OCT-1998;
 09-FEB-1999
 13-APR-2000
 AAA09455;
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Query Match:

Score: Pred.

P X X X X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B

RESULT 12 AAA09455

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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/new protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/new protein, particularly in treating or preventing malignancies in which the HER-2/new oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/new protein (also known as p185 or c-erbB2).
 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; profotocacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target -
 enhancing an immune response to HER-2/\mathrm{neu} protein, particularly useful for treating or preventing cancer, e.g. breast cancer
 or
 New antigen-presenting cells, useful as vaccines for eliciting
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
15
0
0
0
0
 Length:
Matches:
Conservative:
Mismatches:
 Hadwiger
 Indels:
 Human ERBB2 polynucleotide SEQ ID NO 52.
 Gaps:
 JUNC_SEQ3_SEQ4 (1-30) x AAH23392 (1-3768)
 Claim 1; Page 41-46; 49pp; English.
 Rost S,
 BP
 Hand-Zimmermann S;
 ABZ35744 standard; DNA; 3768
 09-JAN-2001; 2001DE-1000588.
 09-JAN-2001; 2001DE-1000588
 0.248
80.00
100.00$
100.00$
50.31$
 (first entry)
 ŝ
 (RIBO-) RIBOPHARMA AG
 WPI; 2002-683450/74.
 2001-476112/51.
 Limmer
(CORI-) CORIXA CORP
 Best Local Similarity:
 P-PSDB; AAB85458
 Percent Similarity:
 DE10100588-A1
 Alignment Scores:
 MA,
 07-FEB-2003
 18-JUL-2002
 Kreutzer R,
 ABZ35744;
 Cheever
 Query Match:
 Pred. No.:
 Ношо
 RESULT 14
셤
 à
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```
with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAH and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the each stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the
 interferon; oncogene; cytokine; Id; developmental;
 invention relates to inhibiting expression of a target gene in a ce introducing at least two oligoribonuclectides (dsRNAI and II), both
 This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded
 Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon
 1915 GACAAGGCTGCCCGCCGCGGGGAGAGCCAGCCTCTGACGTCC 1959
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
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 Conservative:
Mismatches:
 S, Hadwiger P;
 Matches:
 Length:
 Indels:
 Disclosure; Page 43-44; 98pp; German.
 Claim 13; Page 38-39; 100pp; German.
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 Human ERBB2 DNA fragment SEQ ID 52
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 09-JAN-2001; 2001DE-1000587.
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80.00
100.00%
100.00%
50.31%
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 WPI; 2002-742209/81.
 Percent Similarity:
Best Local Similarity:
 Sequence 3768
 DE10100587-C1.
 Homo sapiens.
 Kreutzer R,
 Alignment Scores:
 21-NOV-2002.
 invention.
 ABX09987;
 Query Match:
 ..
No.:
 15
 ABX0998;
 Score:
 Pred.
ò
 g
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das) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRANI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, particularly oncogenes, cytokine genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX0936 ABX10075 represent gene fragments used to illustrate the method of the invention.
```

Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;

| •                                                                                           |  |
|---------------------------------------------------------------------------------------------|--|
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| Length: Matches: Conservative: Mismatches: Indels:                                          |  |
| 0.248<br>80.00<br>100.00%<br>100.00%<br>50.31%                                              |  |
| Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: |  |

JUNC\_SEQ3\_SEQ4 (1-30) x ABX09987 (1-3768)

ŏ qq

Search completed: October 15, 2003, 23:48:38 Job time: 31.4941 secs

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 I21124 Sequence 9
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AX384604 Sequence
AX46729 Sequence
AX481438 Sequence
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AX587649 Sequence
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 Homo sapi
 Sequence
Sequence
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 SUMMARIES
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AX380944
AL591390
AC064803
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2840.777 Million cell updates/sec
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Maximum Match 100%
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Ygapop 10.0, Ygapext
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 Database
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 BASE COUNT
 ORGANISM
 TITLE
JOURNAL
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 FEATURES
 COMMENT
 RESULT
 ORIGIN
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 PAT 18-MAR-2002
 PAT 18-MAR-2002
 Her-2/neu fusion proteins
Patent: WO 0212341-A 28 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualiflers
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Her-2/neu fusion proteins
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90.57%
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AX380944
AX380942
 KEYWORDS
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Jumilicae (17-007-2001) wellcome first Saniger Institute, Hinklou, Cambridgeshire, CBIO 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
nwove.0, 2001 this sequence version replaced gi:16555512.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone and. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TERMEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-355L10 is from ther RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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Mouse DNA linear ROD 17-NOV-2001 Mouse DNA sequence from clone RP23-355L10 on chromosome 11, AL591390
 47794 .47812 .70te-"Sequence from uni-directional primer reads and dGTP big dye terminator reads only." a 47900 c 47689 g 44258 t
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus. musculus chromosome 11, clone RP23-16614
 Submitted (122-178) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 2, 2001 this sequence version replaced gi:12061538.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
 Contact: sequence_submissions@genome.wi.mit.edu
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Matches:
Conservative:
Mismatches:
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 Center project name: L9173
 Mus musculus (house mouse)
Mus musculus
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72.41%
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TITLE
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KEYWORDS
 COMMENT
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Sequencing vector: Plasmid; n/a; 46% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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A NOTE: This a 'working draft' sequence. It currently
Consists of 14 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Direct Submission
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Research Institute, Genetics Division; Tsukiji 5-i-1, Chuo-ku,
Tokyo 104-0045, Japan (E-mail:hksasaki@qanz.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
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AB096614
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 PRI 21-MAY-2003
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 Sasaki, H.

Direct Submission

Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center Submitted (20-NOV-2002) Hiroki Sasaki, Tsukiji 5-1-1, Chuo-ku, Research Institute, Genetics Division; Tsukiji 5-1-1, Chuo-ku, Tokyo 104-0045, Japan (E-mail:hksasaki@gan2.res.ncc.go.jp, Tokyo 108-3-3542-2211(ex.4402), Fax:81-3-3541-2685)

Location/Qualifiers
 Kuwahara,Y., Tanabe,C., Ikeuchi,T., Aoyagi,K., Nishigaki,M., Sakamoto,H., Hoshinaga,K., Yoshida,T., Sasaki,H. and Terada,M. Presence of novel mechanisms other than the BFB cycles in amplification of human oncogene
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 Direct Submission
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center
Submitted (20-NOV-2002) Hiroki Sasaki, Tsukiji 5-1-1, Chuo-ku,
Teksearch Institute, Genetics Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104-0045, Japan (E-mail: hkssaski@gan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
 Kuwahara,Y., Tanabe,C., Ikeuchi,T., Aoyagi,K., Nishigaki,M., Sakamoto,H., Hoshinaga,K., Yoshida,T., Sasaki,H. and Terada,M. Presence of novel mechanisms other than the BFB cycles in amplification of human oncogene
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Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) (ERBB2) gene, complete cds.

AY208911.1 GI:27657999
 Nickerson, D.A.

Direct Submission
Submitted (30-DEC-2002) Genome Sciences, University of Washington, Submitted (30-DEC-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES18478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).

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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

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All repeats were identified using RepeatMasker:
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2 (Dases 1 to 161815)

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Unpublished

S (bases 1 to 16658)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F., Blowslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Colangelo, M., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dewar, K., Dewar, K., Dalaz, J.S., Collymore, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, M., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kanh, L., Karatas, A., Holin, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacKernan, K., McPheeters, R.,
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Homo sapiens chromosome 17, clone CTD-2019C10, complete sequence.
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 Submitted (01-0CT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 1, 2002 this sequence version replaced gi:22597589. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
 - Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
 Only the last 167.6 kb of this clone are being submitted. The remainder overlaps accession number AC097491 [WICGR project
 Web site: http://www-seq.wi.mit.edu
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JOURNAL
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 JOURNAL
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 AUTHORS
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COMMENT

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Consensus quality: 194189 bases at least Q30
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Consensus quality: 194769 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 197308; sum-of-contigs estimation
Quality coverage: 10.95 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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 Pred. No.:
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 2 (bases 1 to 198008)

DOE Joint Genome Institute.

Direct Submission

Submitted (15-MAR-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Homo sapiens (human)
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Immunostimulatory compositions
Patent: US 5976546-A 3 02-NOV-1999;
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Search completed: October 16, 2003, 10:59:54 Job time: 503.208 secs

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GenCore version 5.1.6
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(pdejong@mail.cho.org). Clones be purchased from BACPAC
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 2 LysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGly
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
 618
120
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 Shotgun sequencing of the human transcriptome with ORF expressed
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.I.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
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76 a 119 c 110 g 73 t
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 Email: asimpson@ludwig.org.br
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Location/Qualifiers
 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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 Unpublished
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Emails wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

No SI sequence available.

This clone (DKFZ0686X21213) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@tzpd.de
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
126 c 135 g 84 t
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 Email: bento-soares@ulowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID- 1781731

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
 -----GlnAsnGluAspLeu
 Coordinated Laboratory for Computational Genomics
University of Iowa
175 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
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Fax: 319 335 9565
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42.00%
50.00%
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SOURCE
ORGANISM
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 DEFINITION
 BASE COUNT
 Pred. No.:
 MEDLINE
PUBMED
 ACCESSION
 REFERENCE
 JOURNAL
 BF554233
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 433)
 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Site_2: SmaI; A mini-library was made by cloning products
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0371-250 200-016-allsts1=2000-02-25&t4=1) Seq primer: puc 18 forward High quality sequence stop: 439. Location/Qualifiers
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Crarrhini; Hominidae; Homo.

1 (bases 1 to 450)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., Bordin,S., Costa,F.F.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 BG988031 450 bp mRNA linear EST 13-JUN-2001
MR2-HI1160-110101-005-a06 HI1160 Homo sapiens CDNA, mRNA sequence.
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 \operatorname{Simpson}, \operatorname{A.J.} Shotgun sequencing of the human transcriptome with ORF expressed
 -----GlnAsnGluAspLeu
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 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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VERSION
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 MEDLINE
PUBMED
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 RESULT 9
BG988031
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 EST 21-JUN-2000
 Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Tel: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL2&t2=LL2-CS0049-I81000-202-A06&t3=2000-10-18&t4=1)
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 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
 BE157169 439 bp mRNA linear EST 21-JUN-200 RC3-HT0371-250200-016-all HT0371 Homo sapiens CDNA, mRNA sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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 Contact: Simpson A.J.G.
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50.00$
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 sequence tags
 Simpson, A.J.
 Homo sapiens
 Best Local Similarity:
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 86
 Percent Similarity:
 Alignment Scores:
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 Homo
 Query Match:
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 Pred. No.:
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 BASE COUNT
 ACCESSION
VERSION
 ORGANISM
 JOURNAL
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 KEYWORDS
SOURCE
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 COUNT
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 RESULT 11
BQ828479
 MEDLINE
PUBMED
 ACCESSION
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//clone_lib="Upper | HT1160"
Site_2: Smal; A mini-library was made by cloning products site_2: Smal; A mini-library was made by cloning products site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under liby stringency conditions.

1 127 c 150 g 89 t
 BM720186 466 bp mRNA linear EST 01-MAR-2002 UI-E-EOO-ahz-c-08-0-UI.rl UI-E-EOO Homo sapiens cDNA clone UI-E-EOO-ahz-c-08-0-UI 5', mRNA sequence.
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Seq primer: puc 18 forward
High quality sequence start: 39
High quality sequence start: 39
Location/Qualifiers
 Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 Reverse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 466)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
 University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8256 Fax: 319 335 9565
 259 GACAAGGGTGCCCTGCCGAGCAGCAGCCAGCCCTCTGACGTCC 303
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
 450
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 Email: asimpson@ludwig.org.br
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100.00%
50.00%
 Homo sapiens (human)
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80.00
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Best Local Similarity:
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ORIGIN
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BQ828479
BQ828479
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Hackney, J.A., Charbord, P., Brunk, B.P., Stoeckert, C.J., Lemischka, J.R. and Moore, K.A.
A molecular profile of a hematopoietic stem cell niche
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)
 Princeton University
217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544
 Email: kmoore@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched f
gene products expressed by a hematopoietic stem cell-supporting
stromal cell line, AFT024.
Seq primer: M13Reverse or T7.
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 62
 466
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Mismatches:
Indels:
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 Contact: Moore, Kateri A.
Department of Molecular Biology
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Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Arc.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Argued by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
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50.00%
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 Pred. No.:
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
 Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
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Contact: Dan Fitzpatrick
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Amgen Rat EST Program
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 Pred. No.:
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 Coordinated Laboratory for Computational Genomics
University of Iowa
375 Mewton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 335 8250
Fax: 319 335 8565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seq primer: MI3 Reverse.
 BM720098 561 bp mRNA linear | EST 01-MAR-2002 UI-E-E00-ahz-c-05-0-UI.rl UI-E-E00 Homo sapiens cDNA clone UI-E-E00-ahz-c-05-0-UI 5', mRNA sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 561)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
 561
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 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 Genome Res. 6 (9), 791-806 (1996)
 Location/Qualifiers
 BM720098.1 GI:19039119
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100.00%
50.00%
 Contact: Soares, MB
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 Percent Similarity:
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KEYWORDS
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 AA443351 547 bp mRNA linear EST 03-JUN-1997 8485b05.11 Soares_total_Estus_Nb2HRB_9W Homo sapiens cDNA clone IMAGE:783729 5' similar to qb:M11730 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (HUMAN);, mRNA sequence.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Final: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 Er from Amersham
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Location/Qualifiers
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Publication No. US20020168670A1
GENERAL INFORMATION:
APPLICANT: ECKET, David J.
TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
FILE REFERENCE: IBESO009
CURRENT APPLICATION NUMBER: US/10/109,213
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/09/200,355
PRIOR PILING DATE: 1998-11-25
NUMBER OF SEQ 1D NOS: 4
SOFTWARE: Patentin version 3.1
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame_plus_p2n model

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 of hits satisfying chosen parameters:
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 201 13 US-10-109-213-3
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Maximum Match 100%
Listing first 45 summaries
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 October 16, 2003, 11:08:07
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
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 Minimum DB seq length: 0
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 Title:
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 Score
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 Total number
 OM protein
 Searched:
 Database
 Run on:
 Result
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Conservative: Mismatches: Indels:

Length: Matches:

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| Sequence 2, Application US/09811115
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| APPLICANT: Erickson: Starbheen
| TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
| FILE REFERENCE: GENERT: 034 A
| CURRENT APPLICATION NUMBER: US/09/811,115
| CURRENT APPLICATION NUMBER: US/09/811,115
| PRIOR APPLICATION NUMBER: 60/189,844
| PRIOR FILING DATE: 2000-03-16
| NUMBER: OF SEQ ID NOS: 4
| SOFTWARE: FESTEEQ for Windows Version 4.0
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 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
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 JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-811-115-2 (1-3768)
 APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Dirk
APPLICANT: Cheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: SmithKilne Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US 09/493,480
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 1099-01-28
NUMBER OF SEO ID NOS: 26
SOFTWARE: Patentin Ver: 2.1
 Sequence 9, Application US/09854356 Patent No. US20020177567A1 GENERAL INFORMATION:
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50.00%
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Sequence 5, Application No. US20030143568A1
GENERAL INFORMATION:
APPLICANT: Elizabeth Singer
APPLICANT: Baif Landgraf
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
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APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J
 Sequence 8, Application US/09811123
Sequence 8, Application US/09811123
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
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PRIOR PELLING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
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Matches:
 Indels:
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80.00
100.00%
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 NAME/KEY: CDS
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DB:
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Conservative: Mismatches: Indels:

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Sequence 1, Application US/10313644

Publication No. US2003015711941

GENERAL INFORMATION:
APPLICANT: Gaiger, Martin A.
APPLICANT: Hand-Zimmerman, Susan
TITLE OF INVENTION: MATHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: MAD VIRUS-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.483C3
CURRENT APPLICATION NUMBER: US/10/313,644
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 5
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Matches:
Conservative:
 APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE CO INVENTION: HER. 2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/884,356
CURRENT FILING DATE: 2000-01-09
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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Patent No. US2002017567A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
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 Alignment Scores:
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 LENGTH: 3768
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US-09-854-356-11
 SEQ ID NO 1
 Query Match:
 Pred. No.:
 qq
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 g
 APPLICANT: Cheever, Martin A.

APPLICANT: Cheever, Martin A.

APPLICANT: Cheever, Martin A.

APPLICANT: Foy, Teresa M.

APPLICANT: Monail, Particia D.

APPLICANT: Wedvick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS

TITLE OF INVENTION: COMPOSITION AND METHDOS FOR THE THERAPY AND DIAGNOSIS

TITLE OF INVENTION: COMPOSITION SOURCES

TITLE OF INVENTION: OWNOEST US/09/930,125

CURRENT FILICA DATE: 201-08-14

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LOCATION: (1)...(4763)

O'THER INFORMATION: extracellular domain (ECD) of human HER-2/neu

NAME/KEY: misc_feature

LOCATION: (2026)...(3765)

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NAME/KEY: misc_feature

LOCATION: (2968)...(3765)

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LOCATION: (2968)...(3765)

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Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Hand Zimmerman, Susan
APPLICANT: Cheever, Martin A.
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 Query Match:
 Pred. No.:
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Fri Oct 17 07:47:12 2003

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OTHER INFORMATION: intracellular domain (ICD) of rat HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2188)..(3022)
OTHER INFORMATION: kinase domain (KD) of rat HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2999)..(3796)
OTHER INFORMATION: phosphorylation domain (PD) of rat HER-2/neu
NAME/KEY: misc_feature
LOCATION: (2999)..(31796)
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Best Local Similarity:
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 US-09-854-356-10
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 Query Match:
 Pred. No.:
 Pred. No.:
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 Sequence 117, Application US/09870759
Patent No. US2002017551A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PATENTIN VETSION 3.1
 3955
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 JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-870-759-117 (1-3955)
 JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-854-356-11 (1-3771)
 000
 Sequence 10. Application US/09854356

Patent No. US20020177567A1

GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SEQ TRANKE: Patentin Ver. 2.1
SED ID NO 10
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Mismatches:
Indels:
 Gaps:
 FEATURE: OTHER INFORMATION: rat HER-2/neu cDNA
 0.0205
80.00
100.00%
100.00%
50.00%
 100.00%
50.00%
 TYPE: DNA ORGANISM: Rattus norvegicus
 TYPE: DNA ORGANISM: Rattus norvegicus
 ; LOCATION: (17)..(3799)
; OTHER INFORMATION:
US-09-870-759-117
 Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 US-09-870-759-117
 NAME/KEY: CDS
 Alignment Scores:
 SEQ ID NO 10
LENGTH: 3955
 SEQ ID NO 117
LENGTH: 3955
 US-09-854-356-10
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 FEATURE:
 Query Match:
 Pred. No.:
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Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

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Sequence 117, Application US/09751708A

Sequence 117, Application US/09751708A

Enblication No. US20030157113A1

GENERAL INFORMATION:

APPLICANT: TERMAN. David

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT PELLING DATE: 2002-10-15
PRIOR PAPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-112-28

WINDER OF CENTRE 1999-112-28
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Mismatches:
Indels:
 Length:
 NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 117
LENGTH: 3955
 80.00
100.00%
100.00%
50.00%
 TYPE: DNA ORGANISM: Rattus norvegicus
 0.0205
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junc\_seq3\_seq2res991\_.rnpb

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Sequence 81, Application US/10101510

Sequence 81, Application US/10101510

Sequence 81, Application US/10101510

GENERAL INFORMATION:
APPLICANT: WAN, JACKSON

TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012

CURRENT APPLICATION NUMBER: US/10/101,510

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: 60/276,947

PRIOR PELLING DATE: 2002-03-20

PRIOR PELLING DATE: 2001-03-20

PRIOR PELLING DATE: 2002-03-20

PRIOR PELLING DATE: 2001-03-20
 APPLICANT: SCHOLLER, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, SURFACE RECEPTOR ANTIGEN VACCINES
FILE REPERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
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LENGTH: 4473
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 JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-441-411-5 (1-4473)
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US-10-146-473-32
; Sequence 32, Application US/10146473
 Sequence 5, Application US/09441411 Publication No. US20030008342A1 GENERAL INFORMATION:
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100.00%
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 NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
 0.0234
 TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-101-510-81
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 SEQ ID NO 81
LENGTH: 4473
 Alignment Scores:
US-09-441-411-5
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 Pred. No.:
 Score:
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Sequence 44, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TILLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
 2089 GACAAGGCTGCCCCGCCGAGCAGAGAGCCAGCCTCTGACGTCC 2133
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
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 Conservative:
Mismatches:
 Conservative:
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 APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Goure, Ali
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd
TITLE OF INVENTION: Breast Cancer Antigens
FILE REFERENCE: L00461/70130(JRV)
CURRENT APPLICATION NUMBER: US/10/146,473
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,150
PRIOR APPLICATION NUMBER: US 60/291,150
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin version 3.0
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 Search completed: October 17, 2003, 03:52:37 Job time : 36.0111 secs
Publication No. US20030108888A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Gout, Ivan
APPLICANT: Stockert, Elisabeth
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 Percent Similarity:
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 US-10-207-655-44
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Human heregulin 2
Human herezoneu pr
Human ERBB2 polynu
Human ERBB2 DAA fr
 Human Herz antigen
Human Her -2/neu pr
Human Her -2/neu pr
Human Her -2/neu cD
Human polynucleoti
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 Human tyrosine kin
Human gene express
Breast carcinoma r
Human HER2-neu SEQ
 Human HER-2/neu co
cDNA encoding huma
HER-2/neu oncogene
 Her2-GM-CSF immuno
 Her2 normal form t
 Human tumour antig
HER-2 nucleic acid
Human gene express
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Human Her-2 DNA.
Her-2/neu (ERBB2/c
 Breast cancer asso
Human Her2/Neu enc
HER2 transgene pla
 Mouse Her-2/neu ex
 DNA encoding a wil
 Humanised vector p
 DC8scFv-erbB2EC fu
 Rat neu promoter.
Rat HER-2/neu prot
 Human cDNA differe
 Nucleotide sequenc
 Human ERBB2 polynu
Human ERBB2 DNA fr
Human HER-2 CDNA.
 Sequence encoding cDNA encoding the
 gene.
 Human HER2
 Mouse Her-2/neu extracellular-phosphorylation domain fusion cDNA.
 Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; receptor; mouse; gene therapy; gene; ss.
and is derived by analysis of the total score distribution
 ALIGNMENTS
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ABK14058
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AAH42210
 ABA92251
AAT01590
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 AAD32743
 ABA92250
 ABK10730
 AAQ46083
 ACC50139
 Location/Qualifiers
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 17-JUN-2002 (first entry)
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Match Length
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3768
3768
3768
 3955
 Mus musculus.
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 Key
 ABA92252
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-WODEL-frame+_p2n.model -DEV-x1p
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-DB-N_Geneseq_19Jun03 -OPRT-fastap -SUFFIX-rng -MINMATCH-0_1 -LOOPCL-0
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-DSPV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP=6
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 October 15, 2003, 21:06:28 ; Search time 28.4941 Seconds (without alignments) 2842.104 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

 nucleic search, using frame_plus_p2n model

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 2552756 seqs, 1349719017 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 Xgapop 10.0 , Xgapext
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Delop 6.0 , Delext
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Maximum DB seq
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Perfect score:
 Scoring table:
 Total number
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 Sequence:
 Searched:
 Run on:
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Her-2/neu; oncogene; cancer; tumour; vaccine; tyrosine kinase; Her-2/neu extracellular-phosphorylation domain-TcPO fusion

receptor; TcPO; mouse; gene therapy; gene; ss

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Chimeric

17-JUN-2002 (first entry)

/product= "Her-2/neu ECD-PD-TcP0 fusion"

Location/Qualifiers 1..2781 /\*tag= a

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

(CORI-) CORIXA CORP

Cheever MA, Gheysen D;

03-AUG-2001; 2001WO-US24283. )3-AUG-2000; 2000US-0632507

WO200212341-A2.

```
The present sequence is that of CDNA encoding a fusion between the extracellular domain (BCD) and the phosphorylation domain (BD) murine Her-2/neu oncoprotein is overexpressed in a variety of amplified and the oncoprotein is overexpressed in a variety of human cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor proponosis in breast and ovarian cancers. The invention provides Her-2/neu vercines comprising the fusion proteins or nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acids encoding the proteins or nucleic acid molecules. In preferred fusion proteins, the ECD of Her-2/neu is fused to a immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by carnifecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, uncleic acids, and isolated concern or specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, cells firm a patient. T cells that specifically react with a Her-2/neu concern.
 Her-2/new fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/new extracellular domain fused to Her-2/new intracellular or phosphorylation domain.
 to inhibit the development of cancer in a patient.
 571 A; 855 C; 772 G; 565 T; 0 other;
 /product= "Her-2/neu ECD-PD fusion"
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 Indels:
 (CORI-) CORIXA CORP. (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Disclosure; Fig 23; 141pp; English.
 8.96e-12
150.00
100.00%
90.00%
93.75%
 03-AUG-2001; 2001WO-US24283.
 03-AUG-2000; 2000US-0632507
 Cheever MA, Gheysen D;
 WPI; 2002-241743/29.
P-PSDB; AAM51152.
 Sequence 2763 BP;
 Best Local Similarity:
 WO200212341-A2
 Percent Similarity:
 Alignment Scores:
 14-FEB-2002
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 Score:
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Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
 The present sequence is that of cDNA encoding a fusion between the extracellular domain (ECD) and the phosphorylation domain (PD) murine Her-2/neu oncoprotein (see AAM51151) plus a C-terminal TCPO motif that improves immunogenicity. The Her-2/neu gene is amplified and the oncoprotein is overexpressed in a variety of human cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, uncleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules.
 In preferred fusion proteins, the ECD of Her-2/neu is tused to a large-red fusion proteins, the ECD of Her-2/neu is tused to a large-red fusion proteins, the ECD of Her-2/neu is tused to a large to a dimmune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid serocding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostetae cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
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 Sequence 2781 BP; 574 A; 859 C; 779 G; 569 T; 0 other;
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Conservative:
Mismatches:
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 Disclosure, Fig 25; 141pp; English.
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100.00%
90.00%
93.75%
 phosphorylation domain
 WPI; 2002-241743/29.
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 P-PSDB; AAM51153
 Percent Similarity:
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 Query Match:
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1978 GGCCCTCCAGCCCCATGGACACCTTC 2007

ABA92253 standard; cDNA; 2781 BP

RESULT 2 ABA92253 ABA92253;

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ò

2385 17 0 8 0 0

Conservative: Mismatches: Length: Matches:

0.0564 82.00 68.00% 68.00%

Indels:

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 Best Local Similarity:
 Percent Similarity:
 Alignment Scores:
 Query Match:
 No.
 AAA1481
 RESULT
 ò
 g
 δ
 8
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
 over-expressed in breast and ovarian cancer cells. It was prepd. by PCR amplification of Herz CDNA from a breast cancer cell line and fusion to GM-CSF CDNA. Fusion expression vectors can be used to transfect mammalian and insect cells. The Her2-GM-CSF Call Sion protein is used to generate anti-Her2 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the
 Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in
 A nucleic acid molecule (AAT72725) codes for a fusion protein (AAM19764) comprising granulocyte-macrophage colony stimulating factor (GW-CSF) and Her2, a growth factor receptor that is over-expressed in breast and ovarian cancer cells. It was
 Her2-GM-CSF; granulocyte macrophage colony stimulating factor;
growth factor receptor; oncogene; immunostimulant; cancer;
 Sequence 2385 BP; 488 A; 780 C; 677 G; 440 T; 0 other;
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 Location/Qualifiers
 (ACTI-) ACTIVATED CELL THERAPY INC.
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 Disclosure; Fig 8; 45pp; English.
 /product= GM-CSF
 'product- Her2
 AAT72725 standard; cDNA; 2385
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 95US-0579823
 970..1975
 1976..2359
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 Wu H;
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 .1969
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P-PSDB; AAW19764.
 Laus R, Ruegg CL,
 vertebrate subject
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 Homo sapiens.
 WO9724438-A1
 28-DEC-1995;
 23-DEC-1996;
 17-SEP-1997
 therapy; ss.
 10-JUL-1997
 21
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The present sequence encodes a peptide of wild type erbB-2 receptor protein, where the splicing event occurs. An alternatively spliced variant of erbB-2 receptor protein, designated SPLICE erbB-2 receptor protein, has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting discorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate spLICE erbB-2 are useful for treating cancer. Substances which stimulate spLICE erbB-2 are useful for treating cancer. Substances which stimulate erbB-2 are useful for treating cancer. Substances which stimulate erbB-2 are useful for treating cancer. Substances which stimulate erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone contrain conditions in the degeneration of tissues occurs, such as arthropathy, bone
cancer;
 Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
 SPLICE erbB-2 receptor protein; cell transformation disorder;
 tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
 DNA encoding a wild type erbB-2 receptor protein fragment.
 central nervous system and wound healing.
 Example 2; Fig 3B; 60pp; English.
 BP
 1985 CGCTCGCCCAGCCCC 1999
 AAA14815 standard; cDNA; 69
 99WO-CA00912
 21 GlyProSerSerPro 25
 98US-0165192
 08-AUG-2000 (first entry)
 Siegel PM;
 (UYMC-) UNIV MCMASTER.
 WPI; 2000-303768/26.
 healing; ss.
 P-PSDB; AAY84681
 WO200020579-A1
 Homo sapiens.
 02-OCT-1998;
 01-OCT-1999;
 13-APR-2000.
 Muller WJ,
 AAA14815;
 wound
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4

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The HER2 proto-oncogene encodes a tyrosine kinase receptor, which functions in cellular signal transduction. The HER2 protein is implicated in breast cancer. The HER2 receptor mRNA exists in at least two forms: a normal form and a truncated form. The present sequence is the normal form RNA of HER2. The truncated form RNA sequence of HER2 (AAA62126) encodes a protein associated with increased resistance to the growth inhibiting effects of a monoclonal antibody. Herceptin, used in cancer treatment. The truncated form of the transcript contains unique structures not found in the normal form. The present sequence is predictive of Herceptin-resistant cancer and detection of the present sequence may therefore be used as a method of diagnosing breast cancer. Other diseases which may be identified by using a similar method to detect other RNA molecules are hyperproliferative conditions, Lupus erythematosus, psoriasis, inflammation, cardiovascular disease, pain, arthritis, obesity, trauma, Huntingdon's disease or neurological
 /bound_molety= "her2 normal form transcript bases"
/note= "Forms double-stranded region with bases 137-152
of Her2 normal form transcript"
 Identifying a target nucleic acid sequence predictive of preselected disease states such as a cancerous state, by comparing members of a set of mRNA molecules, from a common gene, containing different sequences
/note= "Forms double-stranded region with bases 172-187 of Her2 normal form transcript" . 154..166
 201
15
0
0
0
 Sequence 201 BP; 34 A; 67 C; 56 G; 44 U; 0 other;
 Conservative:
 Mismatches:
Indels:
 Length:
Matches:
 (1-30) x AAA62125 (1-201)
 Gaps:
 BP,
 Example 2; Fig 3; 38pp; English.
 AAV21727 standard; cDNA; 2125
 99WO-US27710.
 98US-0110024.
 80.00
100.00%
100.00%
50.00%
 /*tag= m
172..187
 0.00542
 (first entry)
 /*tag=
 (ISIS-) ISIS PHARM INC.
 WPI; 2000-400027/34.
 Percent Similarity:
Best Local Similarity:
 JUNC_SEQ3_SEQ2RES991_
 and structures -
 WO200031110-A1
 misc_binding
 22-NOV-1999;
 25-NOV-1998;
 25-NOV-1998;
 Alignment Scores:
 17-AUG-1998
 02-JUN-2000
 stem_loop
 Scker DJ;
 AAV21727;
 116
 Query Match:
 Pred. No.:
 AAV21727
 Score:
 ò
 염
 A X X X E X
 /bound_molety= "Her2 normal form transcript bases"
/note= "Forms double-stranded region with bases 111-117
of Her2 normal form transcript"
 /boind_molety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 121-124
of Her2 normal form transcript"
 /*tag= c
/bound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 74-75
of Her2 normal form transcript"
 /bound_moiety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 58-59
of Her2 normal form transcript"
 /bound_moiety= "her2 normal form transcript"
/note= "Forms double-stranded region with bases 84-90
of Her2 normal form transcript"
 /Dound_molety= "Her2 normal form transcript"
/note= "Forms double-stranded region with bases 78-81
of Her2 normal form transcript"
 Her2; disease prediction; breast cancer; human; tyrosine kinase; ss.
 /bound_moiety= "Her2 normal form transcript bases"
 0000
 Matches:
Conservative:
 Mismatches:
 Length:
 Indels:
 JUNC_SEQ3_SEQ2RES991_ (1-30) x AAA14815 (1-69)
 Gaps:
 Location/Qualifiers
 BP.
 AAA62125 standard; RNA; 201
 Her2 normal form transcript.
 80.00
100.00%
100.00%
50.00%
 0.00147
 (first entry)
 Q
 /*tag= k
137..152
/*tag= 1
 .1117
 121..124
 ..107
 8.18
/*tag=
37.56
/*tag=
58.59
 74..75
/*tag=
 /*tag=
 *tag=
 *tag=
 /*tag=
 /*tag=
 Best Local Similarity:
 Percent Similarity:
 Homo sapiens
 misc_binding
 misc_binding
 misc_binding
 misc_binding
 Alignment Scores:
 20-JUN-2001
 misc_binding
 misc_binding
 misc_binding
 .
 stem_loop
 stem_loop
 stem_loop
 stem_loop
 stem_loop
 AAA62125;
 Query Match:
 Pred. No.:
 RESULT 5
 AAA62125
 g
```

BP

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AA250586 standard; DNA; 2871
 AAZ50586;
 AA250586
 plasmid piTL-hHER2/neu comprises base vector piTL (see AAV21724) and a human HER-2/neu nucleic sequence. piTL-hHER2/neu was used to cavaluate the toxicity of anti-tumour vaccination in rats, and in phase I and phase II trials to evaluate polynucleotide vaccination in advanced breast cancer. Novel humanised vectors, which can be based on piTL, comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells sequence, generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the carpet.
 Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
 /*tag= b
/note= "combined splice and polyA sequences"
1195..1401
 Vector; vaccine; tumour; antigen; plasmid pITL-hHER/neu; human; HER-2/neu; C-erbB-2; breast cancer; ds.
 449 A; 650 C; 598 G; 428 T; 0 other;
 2125
115
0
0
0
 'note- "ColE1 origin of replication"
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 /*tag= a
/product= human HER-2/neu
322..1181
 /*tag= e
/note= "RANTES promoter"
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Example 7; Page 41-42; 125pp; English.
 Cocation/Qualifiers
13..921
 /*tag= c
/note= "SupF gene"
Humanised vector pITL-hHER/neu
 Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
 97WO-US14306
 96US-0023931
 0.0956
80.00
100.00%
100.00%
50.00%
 412..1864
 ..2125
 *tag=
 /*tag=
 Nelson EL, Nelson PJ;
 WPI; 1998-159552/14.
 Sequence 2125 BP;
 Percent Similarity:
Best Local Similarity:
Query Match:
 of the vectors
 misc_feature
 WO9806863-A1
 14-AUG-1997;
 14-AUG-1996;
 Alignment Scores:
 19-FEB-1998
 polyA_site
 Synthetic
 promoter
 ..
0
 Score:
```

1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15

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JUNC\_SEQ3\_SEQ2RES991\_ (1-30) x AAV21727 (1-2125)

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DCB scFv; single-chain variable fragment; erbB2EC; extracellular domain; human; fusion construct; tetramerisation domain; constant domain; heterominbody; multifunctional compound; melanoma; sarcoma; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; antiproliferative; prevention; treatment; malignant; haematopoietic cell; lymphoma; leukaemia; solid tumour; carcinoma; ds.
 DC8scFv-erbB2EC fusion construct containing tetramerisation domain.
 New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis \,
 /*tag= f
//note= "5' end of human IgG3 upper hinge region
with 3 additional nucleotides"
808..924
 *tag= c
|Jabel= DC8scFv_light_chain_variable_region
 tag e
label= DC8scFv_heavy_chain_variable_region
 'product "DC8scFv-erbB2EC fusion protein"
 Ŀ
 g
Human_p53_tetramerisation_domain
 2ett1
 *tag= d
|Tabel= Glycine-Serine-linker_DNA
 Borschert K,
 (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG
 label Short_peptide_linker
 *tag= b
label= Leader_sequence
 /label= erbB2EC_domain
 Location/Qualifiers
10..2865
 Baeuerle PA,
 /label= His_tag
 99WO-EP05416.
 98EP-0114082.
 23-MAY-2000 (first entry)
 2845..2862
 a
 946..2844
 391..435
 75..807
 /*tag=
/label= I
 925..945
 Unidentified.Homo sapiens.
 ..390
 *tag=
 /*tag=
 tag.
 Kufer P, Dreier T,
 WPI; 2000-195265/17.
P-PSDB; AAY44993.
 WO200006605-A2
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 misc_feature
 28-JUL-1999;
 28-JUL-1998;
 10-FEB-2000
 sig_peptide
 Chimeric
Chimeric
 Key
```

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01-NOV-2000; 2000US-0704232.
 Query Match:
 ABK8620
 ò
 a
 The patent discloses heterominibodies which are multifunctional compounds produceable in a mammalian host cell as a secretable and fully functional heterodiamer of two polypeptide chains, where one of the polypeptide chains comprises, a CHI-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different coulypeptides lack an intrinsic affinity for one another and are linked via the constant domains. The heterominibodies have
 cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 The present sequence is a fusion construct comprising DC8 single-chain FV (scrv) fragment at the N-terminus, extracellular domain of human erbB2 at the C-terminus and a tetramerisation domain between them. This construct was prepared to find out whether an Oilsquerisation domain characterised in bacterial expression system is applicable for expression of fully functional and secretable recombinant protein in mammalian host cells. This tetrameric construct was not expressed as secretable and fully functional protein in mammalian cells. Hence general applicability of the tetramerisation domain for oligomerisation strategies in mammalian cells was ruled out.
 Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; ds.
 2797 GACAAGGCTGCCCCGCCGAGCAGCAGCCAGCCCTCTGACGTCC 2841
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 2871 BP; 598 A; 868 C; 834 G; 571 T; 0 other;
 Matches:
Conservative:
 /*tag= a
/product= "HER-2/neu protein"
 Mismatches:
 JUNC_SEQ3_SEQ2RES991_ (1-30) x AAZ50586 (1-2871)
 Length:
 Indels:
 Location/Qualifiers
1..3600
 Example 9; Fig 49; 166pp; English
 Human HER-2/neu coding sequence.
 ВР
 AAA89736 standard; DNA; 3600
 28-JAN-2000; 2000WO-US02164
 99US-0117976
 0.138
80.00
100.00%
100.00%
50.00%
 (first entry)
 melanomas and sarcomas.
 /*tag=
 Best Local Similarity:
 WO200044899-A1
 Percent Similarity:
 Homo sapiens.
 29-JAN-1999;
 Alignment Scores:
 12-JAN-2001
 03-AUG-2000
 AAA89736;
 Query Match:
DB:
 ..
9
 RESULT 8
 AAA89736
 Pred.
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 ò
 g
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cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; parcratic cancer; lymphoma; leukaemia; hepaduavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 The present sequence encodes the human HER-2/neu protein, HER-2/neu is a member of the tyrosine kinase family of receptor-11ke divpoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu diston protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu phosphorylation to treat malignancies such as breast, ovarian, colon, lung and protein cancers, and may be used as an antigen to vaccinate against
 HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
 /*tag= a
/product= "Breast cancer antigen Her2 variant"
 Sequence 3600 BP; 723 A; 1108 C; 1075 G; 694 T; 0 other;
 cDNA encoding human breast cancer antigen, Her2 variant.
 3600
15
0
0
0
 Human; Her2; cytostatic; antiviral; immunostimulant;
 Conservative:
Mismatches:
 Length:
Matches:
 (1-30) x AAA89736 (1-3600)
 Indels:
 Gaps:
 Location/Qualifiers
7..3678
/*tag= a
 Disclosure; Fig 15; 128pp; English.
 ABK86207 standard; cDNA; 3678 BP
 01-NOV-2001; 2001WO-US45626
 100.00%
100.00%
50.00%
(CORI-) CORIXA CORP.
(SMIK) SMITHKLINE BEECHAM.
 P-PSDB; AAB21198, AAB21208
 24-SEP-2002 (first entry)
 Gheysen D;
 WPI; 2000-505976/45
 Percent Similarity:
Best Local Similarity:
 JUNC_SEQ3_SEQ2RES991_
 prostate cancers
 these neoplasias
 WO200240059-A2
 Alignment Scores:
 Homo sapiens
 Cheever MA,
 23-MAY-2002
 ABK86207;
```

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Percent Similarity:
Best Local Similarity:
Query Match:
 P-PSDB; AAW01111
 Homo sapiens.
WO9630514-A1
 28-MAR-1996;
 31-MAR-1995;
 Alignment Scores:
 misc_feature
 03-0CT-1996.
 associated
 AAX01912;
 RESULT 11
 AAX01912
 Score:
 ò
 g
 The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example tumnour cells or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by a diministering a polynuclectide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and leavaemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lenturinses (including human immunodeficiency virus (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present sequence represents the coding sequence of human breast cancer antigen, Her2 variant, used as a target antigen in the method of the invention.
 Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen by a cell, comprises administering a polynucleotide encoding a variant of an antigen -
 /note- "nucleotides 2026-3765 (claim 1) code for HER-2/neu intracellular domain"
 HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; genetic immunisation; tumour; vaccine; vector;
 Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 other;
 3678
15
0
0
0
0
 Matches:
Conservative:
Mismatches:
Indels:
 JUNC_SEQ3_SEQ2RES991_ (1-30) x ABK86207 (1-3678)
 AMERICAN FOUND BIOLOGICAL RES INC.
MINCHEFF M S.
LOUKINOV D I.
 Length:
 Disclosure; Page 128-134; 146pp; English.
 Location/Qualifiers
1..3765
/*tag= b
 Zoubak
 BP
 AAT40739 standard; cDNA; 3768
 0.186
80.00
100.00%
100.00%
50.00%
 DI,
 01-JAN-1997 (first entry)
 Mincheff MS, Loukinov
 WPI; 2002-527524/56.
P-PSDB; AAU98923.
 HER-2/neu oncogene.
 Best Local Similarity:
 ZOUBAK S.
 Percent Similarity:
 Homo sapiens.
 Alignment Scores:
 AAT40739;
 (AMBI-)
 (MINC/)
(LOUK/)
 (ZOUB/)
 Query Match:
 Pred. No.:
 RESULT 10
 Key
 AAT40739
 Score:
g
```

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Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbb2) protein (AAM01111). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Ly8676 val1255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral vector, for genetic immunisation of an animal.
 HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
 DNA encoding HER-2-neu poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/neu oncogene is
 /note= "region which elicits immune response"
 1915 GACAAGGCTGCCCGCCGAGCAAGAGCCAGCCTCTGACGTCC 1959
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 0000
 Conservative:
 Mismatches:
 Length:
Matches:
 JUNC_SEQ3_SEQ2RES991_ (1-30) x AAT40739 (1-3768)
 Indels:
 /product= "HER-2/neu"
/note= "oncogene"
2026..3765
 Location/Qualifiers
1..3768
 Claim 1; Page 49-56; 71pp; English.
 malignancy; treatment; tumour; ss.
 AAX01912 standard; DNA; 3768
 Human HER-2/neu oncogene DNA.
96WO-US01689
 95US-0414417
 0.192
80.00
100.00$
100.00$
50.00$
 21-APR-1999 (first entry)
 ø
 UNIW) UNIV WASHINGTON.
 /*tag=
 /*tag=
 Cheever MA, Disis ML;
 WPI; 1996-455361/45.
```

Dalum I;

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The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGT8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA, and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
 human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
 tumor associated
 Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
 Leach D,
 Antigen-presenting cell; immunogenic; immune response; H[‡]
Oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer
 Nielsen KG, Haaning J,
 Conservative:
 Mismatches:
 /*tag= a
/product= "HER-2/neu protein"
 JUNC_SEQ3_SEQ2RES991_ (1-30) x AAA09455 (1-3768)
 Matches:
 Length:
 Indels:
 Claim 62; Page 187-193; 220pp; English.
 Human HER-2/neu protein encoding DNA.
 Cocation/Qualifiers
 ВР
 Karlsson G;
 AAH23392 standard; DNA; 3768
 21-JAN-2000; 2000US-0177545.
 19-JAN-2001; 2001WO-US01850
 100.00%
100.00%
50.00%
 (first entry)
 0.19280.00
 (MEBI-) M & E BIOTECH AS
 Mouritsen
 WPI; 2000-349917/30
 Birk P,
 Best Local Similarity:
 P-PSDB; AAY92620
 WO200153463-A2
 Percent Similarity:
 Alignment Scores:
 Homo sapiens
 25-SEP-2001
 26-JUL-2001
 Steinaa L,
 Gautam A,
 1915
 AAH23392;
 Query Match:
 No.
 RESULT 13
 Key
 S X C C C C C C C C C X X X L L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X X B L X B
 à
 g
 This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for ellciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
 Use of HER-2/neu polypeptides - for eliciting an immune response to an HER-2/neu associated malignancy, particularly for treating or preventing tumours
 Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cell-associated peptide antigen; foreign epitope; cancer; breast cancer; prostate cancer; ss.
 1915 GACAAGGGTGCCCCGCCGAGAGAGAGACCAGCCCTCTGACGTCC 1959
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
15
0
 Matches:
Conservative:
 Mismatches:
Indels:
 JUNC_SEQ3_SEQ2RES991_ (1-30) x AAX01912 (1-3768)
 Length:
 Human heregulin 2 (Her2) coding sequence.
 Gaps:
 Claim 1a; Column 23-32; 26pp; English
 BP.
 93US-0033644.
93US-0106112.
95US-0414417.
 AAA09455 standard; DNA; 3768
 99WO-DK00525
 98DK-0001261
98US-0105011
 96US-0625101
 96US-0625101
 0.192
80.00
100.00%
100.00%
50.00%
 (first entry)
 (UNIW) UNIV WASHINGTON.
 Cheever MA, Disis ML;
 WPI; 1999-152835/13.
P-PSDB; AAW92406.
 Best Local Similarity:
 WO200020027-A2.
 Percent Similarity:
 17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
 Alignment Scores:
 10-AUG-2000
 Homo sapiens
 05-OCT-1999;
 01-APR-1996;
 05-OCT-1998;
 20-OCT-1998;
US5869445-A
)1-APR-1996;
 13-APR-2000
 09-FEB-1999
 AAA09455;
```

Query Match: DB:

RESULT 12 AAA09455

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.. Q

Score:

15

HER-2/neu;

```
ABX09987;
 Kreutzer
 Query Match:
 No.:
 15
 ABX09987
 Score:
 \mathbf{x} \otimes \mathbf{x} \otimes \mathbf{y} \otimes
 ŏ
 g
 The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/new protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/new protein, particularly in treating or preventing malignancies in which the HER-2/new oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/new protein (also known as pl85 or c-erbb2).
 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target -
 New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
 3768
15
0
0
0
 Conservative:
Mismatches:
 Hadwiger P;
 Length:
Matches:
 JUNC_SEQ3_SEQ2RES991_ (1-30) x AAH23392 (1-3768)
 [ndels:
 Human ERBB2 polynucleotide SEQ ID NO 52.
 Claim 1; Page 41-46; 49pp; English
 ВР
 Rost S,
 Hand-Zimmermann S;
 ABZ35744 standard; DNA; 3768
 09-JAN-2001; 2001DE-1000588
 09-JAN-2001; 2001DE-1000588
 0.192
80.00
100.00%
100.00%
50.00%
 (first entry)
 Ś
 (RIBO-) RIBOPHARMA AG
 WPI; 2002-683450/74.
 Limmer
(CORI-) CORIXA CORP
 WPI; 2001-476112/51
 Best Local Similarity:
 P-PSDB; AAB85458
 Sequence 3768
 Percent Similarity
 Homo sapiens.
 DE10100588-A1
 Alignment Scores:
 Cheever MA,
 07-FEB-2003
 18-JUL-2002
 Kreutzer R,
 ABZ35744;
 Query Match:
 Pred. No.:
 RESULT 14
 Score:
셤
 ò
```

```
with a double-stranded (ds) structure of at most 49 sequential in a cert with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (Si, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the
 The invention relates to inhibiting expression of a target gene in a cell
 Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.
 This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded
 φ
 Inhibiting expression of target genes, e.g. oncogenes, in cells, bintroduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
 0 0
 Conservative:
Mismatches:
Indels:
 ь;
 (1-30) x ABZ35744 (1-3768)
 Matches:
 Hadwiger
 Length:
 Disclosure; Page 43-44; 98pp; German.
Claim 13; Page 38-39; 100pp; German.
 Human ERBB2 DNA fragment SEQ ID 52.
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 ВЪ
 ABX09987 standard; DNA; 3768
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 09-JAN-2001; 2001DE-1000587.
 09-JAN-2001; 2001DE-1000587.
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80.00
100.00%
100.00%
50.00%
 23-JAN-2003 (first entry)
 Limmer S,
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Best Local Similarity:
 JUNC_SEQ3_SEQ2RES991_
 DE10100587-C1
 Homo sapiens.
 Alignment Scores:
 21-NOV-2002.
 ~
 invention.
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```
(ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, particularly oncogenes, cytokine genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX0936-ABX10075 represent gene fragments used to illustrate the method of the invention.
 88888888888888
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Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;

| שדדאווווים ור מכסדמים: |         |               |      |
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| Score:                 | 80.00   | Matches:      | 15   |
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δλ g

Search completed: October 15, 2003, 23:48:35 Job time : 33.4941 secs

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 AX380942 Sequence
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 5777422
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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 160
1 DKGCPAEQRASPLTSQNEDLGPSSPMDSTF 30
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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 DEFINITION
 BASE COUNT
 AL591390/c
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AUTHORS
TITLE
JOURNAL
 ACCESSION
 FEATURES
 COMMENT
 ORIGIN
 LOCUS
 g
 ò
 PAT 18-MAR-2002
 PAT 18-MAR-2002
 Her-2/neu fusion proteins
Patent: WO 0212341-A 30 14-FEB-2002;
CORIXA CORPORATION (US) ; SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualifiers
 S.A. (BE)
 Cheever,M.A. and Gheysen,D.

Her-2/new fusion proteins
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 Cheever, M.A. and Gheysen, D.
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synthetic construct
artificial sequences.
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synthetic construct
artificial sequences.
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90.00%
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 FEATURES
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 SOURCE
 Score:
 g
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אוו 186134 bp DNA linear ROD 17-NOV-2001 Mouse DNA sequence from clone RP23-355L10 on chromosome ll, complete sequence.
 IMPORTANT: This sequence is not the entire insert of clone RP23-355110 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP23-355110 is at 186134 in this sequence. The true right end of clone RP23-438D7 is at 2000 in this
 17991. _.18044
//note="Sequence from uni-directional primer reads and dGTP
big dye terminator reads only."
47794. 47812
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Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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 Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 2, 2001 this sequence version replaced gi:12061538.
 Center: Whitehead Institute/ MIT Center for Genome Research
 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L9173
 186134
20
 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-16G14 Unpublished
 AC064803.4 GI:16596607
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Mus musculus (house mouse)
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Matches:
Conservative:
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72.41%
68.97%
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 Percent Similarity:
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AC064803/c
 Pred. No.:
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
 COMMENT
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Sequencing vector: Plasmid; n/a; 46% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 21076 bases at least Q40
Consensus quality: 21076 bases at least Q30
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Insert size: 197000; agarcose-fp
Quality coverage: 8.5 in Q20 bases; agarose-fp
Quality coverage: 7.8 in Q20 bases;
NOTE: This as "working draft' sequence. It currently
* CONSIST STATE OF The CONTING THE OFFICE OF THE PROPERTY OFFICE OFFIC
 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 f 100 bp
g of 3170 bp in length
f 100 bp
g of 7130 bp in length
 100 bp
of 13991 bp in length
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of 20603 bp in length
 of 21460 bp in length
 100 bp
of 39693 bp in length
100 bp
 of 12575 bp in length
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Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
 Untrock

M Unknown.

Unclassified.

E 1 (bases 1 to 2385)

AS Laus, K., Ruego,C., Landon. and Wu, H.

Immunostimulatory composition

AAL Patent: US 6210662-A 3 03-APR-2001;

Location/Qualifiers

1. 2385

1. 2385

1. 2385
 DNA
 DNA
 Length:
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Laus,R., Ruegg,C.Landon. and Wu,H.
Immunostimulatory method
Patent: US 6080409-A 3 27-JUN-2000;
Location/Qualifiers
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Unclassified.
 Percent Similarity:
Best Local Similarity:
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JOURNAL
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Poung, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 54 Row: c.Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2083)
 Ξ.
 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 BC027080 2083 bp mRNA linear ROD 16-APR-Mus musculus v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/giloblastcma derived oncogene homolog 2, meuro/giloblastcma derived oncogene homolog (avian), mRNA (cDNA clone MGC:38648 IMAGE:5356166), complete cds.
 Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, PH., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDM Library Preparation: Life Technologies, Inc.
CDMA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 Sequencing Center
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 PAT 24-NOV-2000
 PAT 20-DEC-2002
 Springer, C.J. and Marais, R. Surface expression of enzyme in gene directed prodrug therapy Patent: EP 0919622-A 4 02-JUN-1999; CANCER RES CAMPAIGN TECH (GB)
 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
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Identification of disease predictive nucleic acids
Patent: US 6451524-A 3 17-SEP-2002;
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BIOMEDIZINIS (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Pred. No.:
 DEFINITION
 REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
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 PAT 22-JAN-2001
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 Erickson, S. and Schwall, R. Methods of treatment using anti-erbb antibody-maytansinoid conjugates
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Search completed: October 16, 2003, 10:58:43 Job time : 468.208 secs